



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 164100

TO: Patricia Duffy
Location: REM-3B05/3C18
Art Unit: 1645
Saturday, September 03, 2005

Case Serial Number: 09/616247

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Duffy,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

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STIC-Biotech/ChemLib

164100

From: Duffy, Patricia
Sent: Saturday, August 27, 2005 2:10 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

IN RE: 09/616,247

Please search the amino acids sequence of SEQ ID NO:4.
Please run the amino acid sequence of SEQ ID NO:4 against the NA database.
Please include a commercial and interference database search.

Please print out top 100 hits.

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: September 2, 2005, 20:47:12 ; Search time 164 Seconds
(without alignment)
35.374 Million cell updates/sec

Title: US-09-616-247-4

Perfect score: 81

Sequence: 1 QKRAAYDQYGHAAFE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	2	AAW25795
2	81	100.0	15	3	AAW79543
3	81	100.0	15	4	AAW99341
4	81	100.0	15	5	AAU09842
5	81	100.0	15	5	AAU098876
6	81	100.0	15	5	AAE19457
7	81	100.0	15	6	ABR55132
8	81	100.0	16	4	AAW99344
9	81	100.0	16	5	AAU98852
10	81	100.0	16	6	ABR55126
11	81	100.0	118	4	AAU02075
12	81	100.0	131	3	AAH11396
13	81	100.0	131	4	AAW74197
14	81	100.0	131	4	AAW70767
15	81	100.0	131	4	AAW72018
16	81	100.0	340	4	AAU17588
17	81	100.0	340	7	ADB94296
18	81	100.0	341	4	AAU17587
19	81	100.0	341	7	ADB94295
20	81	100.0	373	6	ABM67485
21	81	100.0	376	8	ADR89339
22	81	100.0	376	8	ADR89339
23	81	100.0	378	8	ADN17733
24	81	100.0	378	8	ADS42875
25	81	100.0	380	7	ADF05627

26	81	100.0	380	7	ABOG2494	Abog2494 Klebsiell
27	81	100.0	399	3	AAH11395	Aab11395 E. coli e
28	81	100.0	399	4	AAW74196	Aab74196 OmpA-DnaJ
29	81	100.0	399	4	AAW70766	Aab70766 Expressio
30	81	100.0	399	4	AAW72017	Aay72017 E. coli O
31	81	100.0	459	4	AAU02077	Aau02077 Synthetic
32	81	100.0	476	4	ABG17771	Abg17771 Novel hum
33	74	91.4	365	8	ADS21615	AdS21615 Bacterial
34	73	90.1	344	6	ABP80877	Abp80877 N. gonorr
35	73	90.1	376	6	ADS23054	AdS23054 Bacterial
36	72	88.9	15	2	AAW5446	Aar5446 RA suscep
37	72	88.9	15	2	AAW25796	Aaw25796 Peptide d
38	72	88.9	15	5	AAE19458	Aae19458 Heat shoc
39	72	88.9	15	6	ABR55133	AbR55133 E. coli d
40	69	85.2	382	8	ADN25412	Adn25412 Bacterial
41	69	85.2	384	8	ADS43419	AdS43419 Bacterial
42	67	82.7	376	8	ADR31368	Adr31368 Stress re
43	67	82.7	379	8	ADN24677	Adn24677 Bacterial
44	67	82.7	380	8	ADN21920	Adn21920 Bacterial
45	64.5	79.6	14	2	AAW5445	Aar5445 RA suscep
46	63	77.8	376	8	ADN17394	Adn17394 Bacterial
47	63	77.8	389	8	ADO25512	Ado25512 E. faecali
48	63	77.8	389	8	ADO25510	Ado25510 E. faecali
49	62	76.5	374	8	ADS24625	AdS24625 Bacterial
50	62	76.5	381	7	ABO78428	AbO78428 Pseudomon
51	61	75.3	378	8	ADN25797	Adn25797 Bacterial
52	61	75.3	385	6	ADB10662	AdB10662 Alloiococ
53	60	74.1	375	8	ADS26826	AdS26826 Bacterial
54	60	74.1	376	8	ADS26454	AdS26454 Bacterial
55	59	72.8	358	8	ADN26988	Adn26988 Bacterial
56	58	71.6	332	3	AAW14804	Aag14804 Arabidops
57	58	71.6	367	3	AAW14803	Aag14803 Arabidops
58	58	71.6	379	5	ABR55579	AbR55579 Lactococc
59	58	71.6	379	8	ADS29490	AdS29490 Bacterial
60	58	71.6	385	8	ADS27721	AdS27721 Bacterial
61	58	71.6	456	3	AAW14802	Aag14802 Arabidops
62	57	70.4	369	8	ADS30613	AdS30613 Bacterial
63	57	70.4	377	5	ABR48799	AbR48799 Listeria
64	56	69.1	352	2	AAW22358	S. pneumo
65	56	69.1	362	8	ADN26652	Adn26652 Bacterial
66	56	69.1	378	6	ABU00882	Abu00882 S. pneumo
67	56	69.1	378	6	ABP81556	Abp81556 Streptoco
68	56	69.1	378	8	ADK48132	AdK48132 Streptoco
69	56	69.1	379	5	ABP28852	AbP28852 Streptoco
70	56	69.1	379	5	ADR94852	Adr94852 Novel S.
71	56	69.1	396	5	ABP28853	Abp28853 Streptoco
72	56	69.1	407	8	ADL05213	AdL05213 M. catarr
73	55	67.9	368	3	AAW05934	Aaw05934 Protein d
74	54	66.7	15	2	AAW25798	Aaw25798 Peptide d
75	54	66.7	15	6	ABR55123	AbR55123 E. coli d
76	54	66.7	332	3	AAW48466	Aag48466 Arabidops
77	54	66.7	367	3	AAW48465	Aag48465 Arabidops
78	54	66.7	383	2	AAW34469	Aay34469 Porphorym
79	54	66.7	384	2	AAW34345	Aay34345 Porphorym
80	54	66.7	456	3	AAW48464	Aag48464 Arabidops
81	52	64.2	360	8	ADS21338	AdS21338 Bacterial
82	52	64.2	372	6	ADK44776	AdK44776 Bacterial
83	52	64.2	375	6	ADA33697	Ada33697 Acinetoba
84	52	64.2	376	8	ADN18559	Adn18559 Bacterial
85	50	61.7	297	6	ABU26627	Abu26627 Protein e
86	50	61.7	320	3	AAW30655	Aag30655 Arabidops
87	50	61.7	348	3	AAW30654	Aag30654 Arabidops
88	50	61.7	379	6	ABW70982	Abw70982 Staphyloc
89	49	60.5	295	3	AAW53768	Aag53768 Arabidops
90	49	60.5	295	3	AAW53767	Aag53767 Arabidops
91	49	60.5	323	3	AAW18157	Aag18157 Arabidops
92	49	60.5	323	3	AAW53767	Aag53767 Arabidops
93	49	60.5	350	3	AAW53766	Aag53766 Arabidops
94	49	60.5	350	3	AAW18156	Aag18156 Arabidops
95	49	60.5	370	8	ADS28176	AdS28176 Bacterial
96	48	59.3	423	8	ADS23586	AdS23586 Bacterial
97	47	58.0	284	3	AAW50787	Aag50787 Arabidops
98	47	58.0	292	3	AAW16068	Aag16068 Arabidops

99 47 58.0 309 3 AAG16067 Aag16067 Arabidops
100 47 58.0 337 3 AAG16066 Aag16066 Arabidops

ALIGNMENTS

RESULT 1
AAW25795
ID AAW25795 standard; peptide; 15 AA.

XX AAW25795;
XX
XX 06-APR-1998 (first entry)
XX
XX Peptide dnaJp1 which protects against arthritogenic peptides.
XX
XX dnaJ protein; dnaJp1; adult rheumatoid arthritis; vaccine;
KW arthritogenic peptide; autoimmune disease; systemic immune system;
KW anti-dnaJp1 antibody; passive immunisation;
KW rheumatoid arthritis-susceptibility detection.
XX
XX Escherichia coli.
XX
XX WO9734002-A1.
XX
XX 18-SEP-1997.
XX
XX 20-FEB-1997; 97WO-US002957.
XX
XX 15-MAR-1996; 96US-00618464.
XX

(REGC) UNIV CALIFORNIA.

PA Carson DA, Albani S;

PI WPI; 1997-470892/43.

XX Vaccine for protecting against arthritogenic peptide(s) containing dnaJp1
PT - also determining pre-disposition to rheumatoid arthritis by detecting
PT anti-arthritogenic peptide antibodies.
XX
XX Disclosure; Page 5; 44pp; English.
XX
XX Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from
CC Escherichia coli. One peptide, dnaJp1 (AAW25795) was found to induce
CC relatively strong immune response in seropositive adult rheumatoid
CC arthritis patients. This peptide was used in a vaccine for protecting
CC against arthritogenic peptides. The vaccine contains a carrier, pure
CC dnaJp1 peptide or a recombinant gene expression vector encoding the
CC dnaJp1 peptide. The vaccines are used to prevent rheumatoid arthritis (or
CC other autoimmune diseases). Vaccines can target the arthritogenic
CC peptides before they are presented to the systemic immune system. Anti-
CC dnaJp1 antibodies can also be used for passive immunisation. Antibodies
CC can be used to detect rheumatoid arthritis-susceptibility sequences on
CC HLA or in populations of E. coli in the gastrointestinal tract
XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 2
AA779543
ID AA779543 standard; peptide; 15 AA.
XX
XX AA779543;

XX 15-AUG-2000 (first entry)
XX
XX E. coli dnaJp1 heat shock protein peptide.
XX
XX Antigen presenting cell; T-lymphocyte; T-cell; immunomodulator;
KW autoimmune disease; allergy; cancer; infection; graft rejection;
KW immunotherapy; therapy; major histocompatibility complex; MHC; dnaJp1;
KW heat shock protein.
XX
XX Escherichia coli.
XX
XX WO200023053-A2.
XX
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US024666.
XX
XX 20-OCT-1998; 98US-0105018P.
XX
XX (ALBA/) ALBANI S.
XX
XX Albani S;
XX
XX WPI; 2000-339492/29.
XX
XX New artificial antigen presenting cells useful for isolating and
PT expanding T cells, and modulating T cell responses for the treatment of
PT e.g. autoimmune diseases, allergies.
XX
XX Disclosure; Page 42; 179pp; English.
XX
XX This peptide is derived from Escherichia coli heat shock protein dnaJp1.
CC Novel artificial antigen presenting cells (APC) of the invention comprise
CC antigens, such as the present peptide, that are presented by a major
CC histocompatibility complex (MHC) component for contact with, and
CC recognition by, a T cell receptor. The invention is directed to
CC artificial APC and methods of making APC, which are used to isolate and
CC expand T cell populations and to modulate T cell responses. The invention
CC also provides novel methods for the identification and isolation and
CC antigen-specific T cells. The methods provide for the construction of
CC liposomes containing MHC:peptide complexes, accessory molecules, co-
CC stimulatory molecules, adhesion molecules, and other molecules irrelevant
CC to T cell binding or modulation that are used in the binding of
CC artificial APC to solid support systems that may be used in the retrieval
CC and identification and antigen-specific T cells. Devices and methods are
CC provided for treating conditions that would benefit from modulation of T
CC cell response, e.g. autoimmune disorders (especially type I diabetes
CC mellitus, multiple sclerosis, rheumatoid arthritis, dermatomyositis,
CC juvenile rheumatoid arthritis and uveitis), allergies, cancer, viral
CC infections, and graft rejection
XX
XX Sequence 15 AA;
Query Match 100.0%; Score 81; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 3
AAW99341
ID AAW99341 standard; peptide; 15 AA.
XX
XX AAW99341;
XX
XX 07-DEC-2001 (first entry)
XX
XX Vaccine related MHC ligand peptide SEQ ID NO:444.
XX

Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC; immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal; bactericidal; antiparasitic; fungicidal; cytotostatic; medicine; pharmaceutical; immune disorder; immune deficiency; autoimmune; hypersensitivity; allergy; graft rejection; infection; hormonal disorder; central nervous system disease; cancer; melanoma; anti-melanoma vaccine; human immunodeficiency virus.

OS Homo sapiens.

XX WO200170772-A2.

XX 27-SEP-2001.

XX 22-MAR-2001; 2001WO-FR000872.

XX 23-MAR-2000; 2000FR-00003711.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Klinguer-Hamour C, Corvala N, Beck A, Goetsch L;

XX WPI; 2001-611470/70.

Stabilized pharmaceutical containing N-terminal glutamic acid or glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt with strong acid.

PS Claim 9; Page 107; 149pp; French.

XX The present invention describes a pharmaceutical compound (I) that contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in the form of an addition salt with a strong, physiologically acceptable acid (II). Also described are: (a) a pharmaceutical composition containing at least one (I); (b) a vaccine containing at least one (I) where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a method for in vitro diagnosis of diseases associated with the presence of (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process for preparing (I). (I) has immunomodulator, endocrine, antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and cycostatic activities. (I) are useful, in human or veterinary medicine, in pharmaceutical compositions (for treating immune disorders, e.g. immune deficiency, autoimmune states, hypersensitivity, allergy, graft rejection, infection, hormonal disorders and central nervous system diseases), also where (I) is a MHC ligand (Ia) in vaccines for treatment or prevention of: (i) viral, bacterial, parasitic or fungal infections; or (ii) of cancers. A particular application is in anti-melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases associated with interactions between MHC and (I), e.g. melanoma and human immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides which can be used in pharmaceutical compounds from the present invention

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 1 QKRAAYDQYGHAAFE 15

RESULT 4

AAU09842
ID AAU09842 standard; peptide; 15 AA.

XX AAU09842;

XX 26-FEB-2002 (first entry)

XX E.coli dnaJp1 heat shock protein-derived peptide.

XX

Antigenic; antidiabetic; neuroprotective; antirheumatic; antiarthritic; dermatological; immunosuppressive; ophthalmological; antiallergic; cytostatic; virucide; antibacterial; artificial antigen presenting cell; liposome; major histocompatibility complex; MHC; T cell; allograft; cytokine production; T-helper 2 response; transplantation therapy; autoimmune disease; type 1 diabetes mellitus; multiple sclerosis; rheumatoid arthritis; dermatomyositis; juvenile rheumatoid arthritis; uveitis; allergy; cancer; infection; dnaJp1 heat shock protein.

XX Escherichia coli.

XX WO200180833-A1.

XX 01-NOV-2001.

XX 20-APR-2000; 2000WO-IT000161.

XX 20-APR-2000; 2000WO-IT000161.

XX (ALBA/) ALBANI S.

XX Albani S;

XX WPI; 2002-055316/07.

New artificial antigen presenting cell, useful for modulating T cell response for treating allergies and cancers, comprises liposome, major histocompatibility complex, antigen and accessory molecule components.

PS Disclosure; Page 46; 195pp; English.

XX The invention relates to an artificial antigen presenting cell (I) comprising liposome, major histocompatibility complex (MHC), antigen and accessory molecule components. (I) is used in methods for the following: (1) identifying T cells specific for an antigen of interest; (2) isolating T cells specific for an antigen of interest; (3) modulating T cell response; (4) characterising the functional state of antigen-specific T cells; (5) treating a condition in a subject which would be benefited by altering the functional pattern of cytokine production by certain antigen-specific T cells to increase T-helper (Th) 2 response and/or decrease Th1 response; (6) identifying antigen-specific T cells specific for epitopes on a graft donor's tissue likely to elicit graft versus host rejection response; and (7) treating a recipient mammal to reduce rejection of allografts in a transplantation therapy regime. Method (5) is useful for treating autoimmune disease such as type 1 diabetes mellitus, multiple sclerosis, rheumatoid arthritis, dermatomyositis, juvenile rheumatoid arthritis or uveitis. Alternatively it is useful for treating allergy due to allergens such as dust, animal skin bypass products, vegetables, fruits, pollen or chemicals, cancer, viral infection, bacterial infection. Addition of the accessory molecules, as well as co-stimulatory molecules, and other proteins in proper orientation in the liposomes allow for substantially improved binding association and manipulation of T cells which is very important in the identification and stimulation of antigen-specific T cells. The present sequence represents E.coli dnaJp1 heat shock protein-derived peptide used in the method of the invention

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 1 QKRAAYDQYGHAAFE 15

RESULT 5

AAU98876

ID AAU98876 standard; peptide; 15 AA.

XX AAU98876;

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XX DT 22-AUG-2002 (first entry)
XX DE E. coli DNAJ PI immunogenic peptide.
XX KW Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
XX KW cytostatic; antiinflammatory; antibacterial; antiarthritic; human;
XX KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
XX KW infectious disease; inflammatory bowel disease; cancer; HDJ2;
XX KW mucosal tolerisation; DNA vaccination; anergy induction.
XX OS Escherichia coli.
XX PN WO200236611-A2.
XX PD 10-MAY-2002.
XX PF 31-OCT-2001; 2001WO-US045344.
XX PR 01-NOV-2000; 2000US-0245181P.
XX XX (REGC ) UNIV CALIFORNIA.
XX PA (MART/) MARTINI A.
XX XX Martini A, Albani S, Carson DA, Prakken BJ;
XX PI WPI; 2002-489999/52.
XX DR New immunomodulatory peptides from heat shock proteins, useful for
XX XX treating immunological disorder in subjects such as humans, e.g.
XX PT autoimmune disease (e.g. arthritis), infectious disease, inflammatory
XX PT bowel disease or cancer.
XX XX Example 8; Page 53; 84pp; English.
XX PS This invention relates to the use of a peptide, which is an immunogenic
XX CC portion derived from a dnaJ heat shock protein (hsp) in modulating an
XX CC immune response in a subject. The peptides of the invention may have
XX CC immunomodulatory, cytostatic, antiinflammatory, antibacterial or
XX CC antiarthritic properties and can stimulate expression of interleukins,
XX CC tumour necrosis factor and transforming growth factor beta. The
XX CC immunogenic peptide is useful for modulating (i.e. augmenting/inducing or
XX CC reducing/inhibiting) an immune response in a subject having an
XX CC immunological disorder (e.g. autoimmune disease such as arthritis or
XX CC articular juvenile idiopathic arthritis), an infectious disease, an
XX CC inflammatory bowel disease or cancer. The immunogenic peptide of the
XX CC invention is also useful for modulating immunoeffector cell
XX CC responsiveness in a subject. The immunogenic peptide is particularly
XX CC useful for treating the above-mentioned diseases in mammals, e.g. cat,
XX CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
XX CC general, the peptide is useful in methods involving mucosal tolerisation,
XX CC DNA vaccination, anergy induction or active immunisation. The present
XX CC sequence represents the E.coli DNAJ PI immunogenic peptide of the
XX CC invention
XX SQ Sequence 15 AA;
Query Match 100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
DB 1 QKRAAYDQYGHAAFE 15
RESULT 6
ID AAE19457 standard; peptide; 15 AA.
XX AAE19457;
XX AC AAE19457;
XX XX 31-MAY-2002 (first entry)

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XX DE Human heat shock protein (hsp) dnaJPI peptide.
XX KW Human; human leukocyte antigen; HLA; DR-binding peptide; therapy;
XX KW stress protein; major histocompatibility complex; MHC; antiulcer;
XX KW type I diabetes; scleroderma; heat shock protein; hsp; vitiligo;
XX KW rheumatoid arthritis; lupus erythematosus; myasthenia gravis; tumour;
XX KW ulcerative colitis; infectious disease; haemostatic; nephroticosis;
XX KW polymyositis; chronic active hepatitis; primary biliary cirrhosis;
XX KW pernicious anaemia; autoimmune thyroiditis; Sjogren's syndrome; cancer;
XX KW Grave's disease; autoimmune disease; multiple sclerosis; hepatotropic;
XX KW inflammatory bowel disease; Goodpasture's syndrome; neuroprotective;
XX KW antimicrobial; immunosuppressive; dermatological; antiinflammatory;
XX KW antiinfertility; idiopathic Addison's disease; cytostatic.
XX OS Homo sapiens.
XX PN WO200212286-A2.
XX PD 14-FEB-2002.
XX PF 08-AUG-2001; 2001WO-US041656.
XX PR 09-AUG-2000; 2000US-0224104P.
XX PR 06-APR-2001; 2001US-00828574.
XX XX (UYCA-) UNIV CALIFORNIA SAN DIEGO.
XX PI Albani S, Prakken BJ;
XX XX WPI; 2002-227137/28.
XX DR Novel human leukocyte antigen pan DR-binding peptide, useful for treating
XX PT immune mediated diseases and conditions, has a fragment of stress protein
XX PT that binds to major histocompatibility complex class II molecules.
XX PS Claim 9; Page 45; 68pp; English.
XX XX The invention relates to human leukocyte antigen (HLA) pan DR-binding
XX CC peptide comprising a fragment of a stress protein that binds to one or
XX CC more major histocompatibility complex (MHC) class II molecules. The
XX CC invention also relates to heat shock protein (hsp) peptides. The peptides
XX CC of the invention and thr immunomodulating composition comprising these
XX CC peptides are useful for modulating, treating or preventing an immune-
XX CC mediated disease in a mammalian subject e.g. human, having or at risk of
XX CC having a disease including autoimmune disease, multiple sclerosis (MS),
XX CC rheumatoid arthritis, lupus erythematosus, myasthenia gravis, type I
XX CC diabetes, scleroderma, ulcerative colitis, cancer (e.g. melanoma,
XX CC lymphoma, leukaemia, lung, liver, kidney, brain, bladder solid tumours,
XX CC retinoblastoma, sarcoma and connective tissue cancers) and infectious
XX CC diseases. The peptides of the invention are also useful for screening
XX CC peptides or analogues that modulate pathogenic immune response. These
XX CC peptides are useful for treating autoimmune diseases or disorders
XX CC including Sjogren's syndrome, polymyositis, chronic active hepatitis,
XX CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
XX CC anaemia, autoimmune thyroiditis, vitiligo, idiopathic Addison's disease,
XX CC gluten-sensitive enteropathy, Grave's disease, inflammatory bowel
XX CC disease, autoimmune neutropaenia, idiopathic thrombocytopenia purpura,
XX CC pemphigus vulgaris, autoimmune infertility, Goodpasture's syndrome,
XX CC bullous pemphigoid, discoid lupus and dense deposit disease. The present
XX CC sequence is human hsp dnaJPI peptide used in the exemplification of the
XX CC invention
XX SQ Sequence 15 AA;
Query Match 100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
DB 1 QKRAAYDQYGHAAFE 15

```

RESULT 7
ABR55132
ID ABR55132 standard; peptide; 15 AA.
XX
AC ABR55132;
XX
DT 03-JUL-2003 (first entry)
XX
DE E. coli DnaJp1 antigen-specific epitope peptide.
XX
XX Antigen-specific epitope; immune response; T cell; cytokine;
KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
KW cytosolic; antithyroid; anti-asthmatic; immunosuppressive;
KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
KW antiallergic; dermatological; antipsoriatic.
XX
OS Escherichia coli.
XX
PN WO2003026579-A2.
XX
PD 03-APR-2003.
XX
PF 25-SEP-2002; 2002WO-US030578.
XX
PR 25-SEP-2001; 2001US-0325499P.
XX
PR 11-DEC-2001; 2001US-0339284P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Albani S, Martins A;
XX
XX WPI; 2003-430097/40.
XX
XX
XX Modulating an immune response in a subject having an immune-related
PT disorder, e.g. arthritis by administering an antigen-specific epitope and
PT a cytokine or an agent that effects cytokine activity or expression.
XX
XX Disclosure; Page 9; 41pp; English.
XX
XX The invention relates to a novel method for modulating an immune response
CC in a subject having an immune-related disorder. The method comprises: (a)
CC administering an antigen-specific epitope, where administration provides
CC epitope-specific T cell immune modulation; and (b) administering a
CC cytokine, an agent that effects cytokine activity or expression, or an
CC anticytokine therapy. The method of the invention has antiarthritic,
CC antidiabetic, neuroprotective, anti-inflammatory, cytosolic,
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,
CC dermatological, and antipsoriatic activity. The method is useful for
CC modulating an immune response in a subject having an immune-related
CC disorder. The present sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15
RESULT 8
AAM99344
ID AAM99344 standard; peptide; 16 AA.
XX
AC AAM99344;
XX
XX 07-DEC-2001 (first entry)
DT
XX

DE Vaccine related MHC ligand peptide SEQ ID NO:447.
XX
KW Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
KW human immunodeficiency virus.
XX
OS Homo sapiens.
XX
PN WO200170772-A2.
XX
PD 27-SEP-2001.
XX
PF 22-MAR-2001; 2001WO-FR000872.
XX
PR 23-MAR-2000; 2000FR-00003711.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
XX
XX WPI; 2001-611470/70.
XX
XX Stabilized pharmaceutical containing N-terminal glutamic acid or
PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
PT with strong acid.
XX
XX Claim 9; Page 107; 149pp; French.
XX
XX The present invention describes a pharmaceutical compound (I) that
CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
CC the form of an addition salt with a strong, physiologically acceptable
CC acid (II). Also described are: (a) a pharmaceutical composition
CC containing at least one (I); (b) a vaccine containing at least one (I)
CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
CC method for in vitro diagnosis of diseases associated with the presence of
CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
CC cytostatic activities. (I) are useful, in human or veterinary medicine,
CC in pharmaceutical compositions (for treating immune disorders, e.g.
CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
CC rejection, infection, hormonal disorders and central nervous system
CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
CC infections; or (ii) of cancers. A particular application is in anti-
CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
CC associated with interactions between MHC and (I), e.g. melanoma and human
CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides
CC which can be used in pharmaceutical compounds from the present invention
XX
SQ Sequence 16 AA;
Query Match 100.0%; Score 81; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15
RESULT 9
AAU98852
ID AAU98852 standard; peptide; 16 AA.
XX
AC AAU98852;
XX
XX 22-AUG-2002 (first entry)
DT
XX

```

DE E.Coli DNAJ 61 immunogenic peptide.
XX
KW Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
KW cytosolic; antiinflammatory; antibacterial; antiarthritic;
KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
KW infectious disease; inflammatory bowel disease; cancer;
KW mucosal toleration; DNA vaccination; anergy induction.
XX
OS Escherichia coli.
XX
PN WO200236611-A2.
XX
PD 10-MAY-2002.
XX
PF 31-OCT-2001; 2001WO-US045344.
XX
PR 01-NOV-2000; 2000US-0245181P.
XX
XX (REGC ) UNIV CALIFORNIA.
PA (MART/) MARTINI A.
XX
XX Martini A, Albani S, Carson DA, Prakken BJ;
PI WPI; 2002-489999/52.
XX
DR New immunomodulatory peptides from heat shock proteins, useful for
PT treating immunological disorder in subjects such as humans, e.g.
PT autoimmune disease (e.g. arthritis), infectious disease, inflammatory
PT bowel disease or cancer.
XX
PS Claim 4; Page 55; 84pp; English.
XX
CC This invention relates to the use of a peptide, which is an immunogenic
CC portion derived from a dnaJ heat shock protein (hsp) in modulating an
CC immune response in a subject. The peptides of the invention may have
CC immunomodulatory, cytosolic, antiinflammatory, antibacterial or
CC antiarthritic properties and can stimulate expression of interleukins,
CC tumour necrosis factor and transforming growth factor beta. The
CC immunogenic peptide is useful for modulating (i.e. augmenting/inducing or
CC reducing/inhibiting) an immune response in a subject having an
CC immunological disorder (e.g. autoimmune disease such as arthritis or
CC articular juvenile idiopathic arthritis), an infectious disease, an
CC inflammatory bowel disease or cancer. The immunogenic peptide of the
CC invention is also useful for modulating immunoeffector cell
CC responsiveness in a subject. The immunogenic peptide is particularly
CC useful for treating the above-mentioned diseases in mammals, e.g. cat,
CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
CC general, the peptide is useful in methods involving mucosal toleration,
CC DNA vaccination, anergy induction or active immunisation. The present
CC sequence represents an E. coli DNAJ immunogenic peptide of the invention
XX
SQ Sequence 16 AA;
Query Match 100.0%; Score 81; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
DB 1 QKRAAYDQYGHAAFE 15
|||||
RESULT 10
ABR55126
ID ABR55126 standard; peptide; 16 AA.
XX
AC ABR55126;
XX
XX 03-JUL-2003 (first entry)
DT
DE E. coli dnaJ61 antigen-specific epitope peptide.
XX
XX Antigen-specific epitope; immune response; T cell; cytokine;
KW

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KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
KW cytosolic; antithyroid; anti-asthmatic; immunosuppressive;
KW antipsoriatic; anti-ulcer; antianaemic; cardiac; respiratory;
KW antiallergic; dermatological; antipsoriatic.
XX
OS Escherichia coli.
XX
PN WO2003026579-A2.
XX
PD 03-APR-2003.
XX
PF 25-SEP-2002; 2002WO-US030578.
XX
PR 25-SEP-2001; 2001US-0325499P.
PR 11-DEC-2001; 2001US-0339284P.
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX Albani S, Martins A;
PI WPI; 2003-430097/40.
XX
DR Modulating an immune response in a subject having an immune-related
PT disorder, e.g. arthritis by administering an antigen-specific epitope and
PT a cytokine or an agent that effects cytokine activity or expression.
XX
PS Disclosure; Page 9; 41pp; English.
XX
CC The invention relates to a novel method for modulating an immune response
CC in a subject having an immune-related disorder. The method comprises: (a)
CC administering an antigen-specific epitope, where administration provides
CC epitope-specific T cell immune modulation; and (b) administering a
CC cytokine, an agent that effects cytokine activity or expression, or an
CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
CC ulcer, antianaemic, cardiac, respiratory general, antiallergic,
CC dermatological, and antipsoriatic activity. The method is useful for
CC modulating an immune response in a subject having an immune-related
CC disorder. The present sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 16 AA;
Query Match 100.0%; Score 81; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
DB 1 QKRAAYDQYGHAAFE 15
|||||
RESULT 11
AAU02075
ID AAU02075 standard; protein; 118 AA.
XX
AC AAU02075;
XX
XX 07-SEP-2001 (first entry)
DT
DE Synthetic autoantigen shHSP/RA.
XX
KW shGLP/RA; immunogenic epitope cluster; IEC;
KW synthetic human 60kDa heat shock protein; HSP60; HSP65; EcDNAJ;
KW autoantigen; autoimmune disease; multiple sclerosis;
KW rheumatoid arthritis; insulin-dependent diabetes mellitus;
KW myasthenia gravis; uveitis; autoimmune hepatitis; thyroiditis; insulinitis;
KW orchitis; idiopathic thrombocytopenic purpura; inflammatory disease;
KW Crohn's disease; ulcerative colitis;
KW Mycobacterium tuberculosis heat shock protein 65; Escherichia coli DNA J.
XX
OS Synthetic.

```

OS Homo sapiens.
 OS Escherichia coli.
 OS Mycobacterium tuberculosis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 116
 FT /label= OTHER
 FT /note= "Other= STOP"
 XX
 PN WO200131037-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-IL000688.
 XX
 PR 27-OCT-1999; 99IL-00132611.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Ben-Nun A, Kerliero De Rosbo N, Sappller GP;
 XX
 DR WPI: 2001-300515/31.
 DR N-PSDB; AAS04836.
 XX
 PT Novel synthetic human target autoantigen gene useful for treating
 PT autoimmune diseases such as multiple sclerosis, insulin-dependent
 PT diabetes mellitus, rheumatoid arthritis, myasthenia gravis, and uveitis.
 XX
 PS Claim 176; Fig 53; 182pp; English.
 XX
 CC The sequence represents sHSP/RA containing immunogenic epitope clusters
 CC (IEC) from Mycobacterium tuberculosis heat shock protein 65, Escherichia
 CC coli DNA J and human heat shock protein 60. The synthetic human target
 CC autoantigen genes of the invention comprise sequences coding for at least
 CC 2 IECs of autoantigen(s) related to a specific autoimmune disease. The
 CC synthetic human target autoantigen genes are useful for treating
 CC autoimmune diseases such as multiple sclerosis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, myasthenia gravis, uveitis,
 CC autoimmune hepatitis, thyroiditis, insulinitis, orchitis, idiopathic
 CC thrombocytopenic purpura, and inflammatory diseases (Crohn's disease,
 CC ulcerative colitis). The synthetic human target autoantigen genes are
 CC also useful for diagnosis and/or monitoring the progression of the
 CC autoimmune disease
 XX
 SQ Sequence 118 AA;
 Query Match 100.0%; Score 81; DB 4; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 Db |||||
 99 QKRAAYDQYGHAAFE 113
 RESULT 12
 AAB11396
 ID AAB11396 standard; protein; 131 AA.
 XX
 AC AAB11396;
 XX
 DT 22-FEB-2001 (first entry)
 XX
 DE E. coli expression plasmid PUBS520-PIN-J-Domain encoded protein.
 XX
 KW Eukaryotic protein; protease; interferon; antibody; hormone;
 KW disulfide bridge.
 XX
 OS Escherichia coli.
 OS Synthetic.
 XX
 PN EP1048732-A1.
 XX

PD 02-NOV-2000.
 XX
 PF 26-APR-1999; 99EP-00107412.
 XX
 PR 26-APR-1999; 99EP-00107412.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 DR WPI: 2000-674185/66.
 DR N-PSDB; AAC66072.
 XX
 PT Preparation of water-soluble eukaryotic polypeptides with disulfide
 PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
 PT presence of arginine or amide compound.
 XX
 PS Example 3; Page 17; 40pp; German.
 XX
 CC This invention describes a novel preparation of a water-soluble,
 CC naturally occurring eukaryotic polypeptide containing two or more
 CC cysteine units bound via a disulfide bridge which comprises cultivation
 CC of prokaryotic cells in the presence of arginine or an amide compound.
 CC The method is useful for the preparation of eukaryotic proteins e.g.
 CC proteases, interferons, protein hormones, antibodies or antibody
 CC fragments (e.g. a single chain Fv fragment that binds to thyroid
 CC stimulating hormone). It is especially useful for preparing proteins with
 CC more than five disulfide bridges, e.g. recombinant plasminogen activator
 CC (rPA). The technique is simple and does not require in vitro after-
 CC treatment, such as the removal of inclusion bodies, reduction or
 CC nitrization
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 81; DB 3; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 Db |||||
 84 QKRAAYDQYGHAAFE 98
 RESULT 13
 AAB74197
 ID AAB74197 standard; protein; 131 AA.
 XX
 AC AAB74197;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE OmpA-J domain fusion protein.
 XX
 KW Molecular chaperone; OmpA signal sequence; J domain; DnaJ.
 XX
 OS Unidentified.
 XX
 PN EP1077262-A1.
 XX
 PD 21-FEB-2001.
 XX
 PF 24-JUL-2000; 2000EP-00115839.
 XX
 PR 29-JUL-1999; 99EP-00114811.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
 XX
 DR WPI: 2001-246712/26.
 DR N-PSDB; AAF77804.
 XX
 PT Producing naturally folded eukaryotic proteins e.g. antibodies,
 PT interferon, hormones or proteases that contain two or several cysteines
 PT linked by disulfide bridges comprises co-expression of a molecular

PT chaperone.
XX
PS Disclosure; Page 14; 35pp; English.
XX
CC The present invention relates to a method for production of a naturally
CC folded eukaryotic protein containing two or more cysteines linked by
CC disulfide bridges. The method comprises co-expression and secretion into
CC the periplasm of a molecular chaperone via an expression vector coding
CC for the chaperone. The expression vector also encodes a signal sequence.
CC The method is useful for producing a naturally folded eukaryotic protein
CC such as an antibody, antibody fragment, interferon, protein hormone or a
CC protease containing two or several cysteines linked by disulfide bridges.
CC The present sequence is a fusion protein composed of the OmpA signal
CC sequence and the J domain of DnaJ. This sequence was used in the method
CC of the present invention
XX
SQ Sequence 131 AA;

Query Match 100.0%; Score 81; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDOYGHAAFE 15
Db 84 QKRAAYDOYGHAAFE 98
|||||
QY 1 QKRAAYDOYGHAAFE 15
Db 84 QKRAAYDOYGHAAFE 98
|||||

RESULT 15
AAY72018
ID AAY72018 standard; protein; 131 AA.
XX
AC AAY72018;
XX
XX 28-MAR-2001 (first entry)
XX
XX E. coli OmpA-J domain fusion protein encoded by PUBS520-pIN-J-domain.
XX
XX Secreted protein; chaperone; interferon; protease; hormone;
KW fusion protein; naturally folded protein; lac-Ipp promoter; DnaJ;
KW heat shock protein; HSP; outer membrane protein A; OmpA; J domain.
XX
XX Escherichia coli.
XX
XX EP1054063-A2.
XX
XX 22-NOV-2000.
XX
XX 19-APR-2000; 2000EP-00108505.
XX
XX 26-APR-1999; 99EP-00107412.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Ambrosius D, Rudolph R, Schaeffner J, Schwarz B;
XX
XX WPI; 2001-033777/05.
DR N-PSDB; AAD02210.
XX
XX Producing water-soluble, naturally folded, and secreted eukaryotic
PT polypeptide, involves culturing prokaryotic cells containing an
PT expression vector encoding the polypeptide in the presence of arginine or
PT a specific compound.
XX
XX Example 3; Page 17; 35pp; English.
XX
XX The patent discloses a method for the production of a water-soluble,
CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.
CC The method involves culturing the prokaryotic cells, containing an
CC expression vector encoding the desired protein and the prokaryotic signal
CC sequence, in the presence of an additive, e.g., L-arginine. The signal
CC sequence mediates the secretion of the desired protein into the
CC periplasm, where folding of the protein takes place. The prokaryotic cell
CC also contains an expression vector encoding a molecular chaperone, e.g.,
CC DnaJ and heat shock protein 25 (HSP25). The simultaneous co-
CC overexpression and co-secretion of molecular chaperones in the periplasm
CC improves the yield of functionally folded protein. The above method
CC recombinantly produces a high yield of eukaryotic secreted proteins in
CC prokaryotes. The method is useful for producing eukaryotic proteins such
CC as an antibody, antibody fragment, interferon, protein hormone or a
CC protease. The present sequence is an Escherichia coli outer membrane
CC protein A (OmpA) signal sequence-J domain fusion protein encoded by
CC PUBS520-pIN-J-domain. The plasmid, PUBS520-pIN-J-domain, also contains
CC the lac-Ipp promoter and the Ipp terminator. The periplasmic co-secretion
CC of J domain, which is the N-terminal portion of the DnaJ, facilitates the
CC folding of the desired secreted protein
XX

PT chaperone.
XX
PS Disclosure; Page 14; 35pp; English.
XX
CC The present invention relates to a method for production of a naturally
CC folded eukaryotic protein containing two or more cysteines linked by
CC disulfide bridges. The method comprises co-expression and secretion into
CC the periplasm of a molecular chaperone via an expression vector coding
CC for the chaperone. The expression vector also encodes a signal sequence.
CC The method is useful for producing a naturally folded eukaryotic protein
CC such as an antibody, antibody fragment, interferon, protein hormone or a
CC protease containing two or several cysteines linked by disulfide bridges.
CC The present sequence is a fusion protein composed of the OmpA signal
CC sequence and the J domain of DnaJ. This sequence was used in the method
CC of the present invention
XX
SQ Sequence 131 AA;

Query Match 100.0%; Score 81; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDOYGHAAFE 15
Db 84 QKRAAYDOYGHAAFE 98
|||||
QY 1 QKRAAYDOYGHAAFE 15
Db 84 QKRAAYDOYGHAAFE 98
|||||

RESULT 14
AAB70767
ID AAB70767 standard; protein; 131 AA.
XX
AC AAB70767;
XX
XX 18-MAY-2001 (first entry)
XX
XX Expression plasmid PUBS520-pIN-J-domain protein.
XX
XX Chaperone protein; periplasm; antibody production; protein production;
KW interferon production; protease production.
XX
XX Escherichia coli.
OS Synthetic.
XX
XX EP1077263-A1.
PN
XX 21-FEB-2001.
PD
XX 29-JUL-1999; 99EP-00114811.
XX
XX 29-JUL-1999; 99EP-00114811.
PR
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA
XX WPI; 2001-204356/21.
DR N-PSDB; AAF61191.
XX
XX Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by
PT simultaneous expression of a chaperone protein, allows simple recovery
PT from periplasm or medium.
XX
XX Disclosure; Page 15; 36pp; German.
XX
XX This invention describes a novel method for preparing a naturally folded
CC eukaryotic polypeptide (I) that contains two or more disulfide-bridged
CC Cys residues by culturing prokaryotic cells that contain an expression
CC vector for (I) including a prokaryotic signal sequence at its N-terminus
CC and a nucleic acid (II) that secretes a chaperone protein (III) into the
CC periplasm. (I) is secreted into the periplasm or medium; the signal
CC peptide is then cleaved and (I) isolated from the periplasm or medium.
CC The method is used for production of antibody, interferon, protein
CC hormone or protease. Expression of (III) increases the yield of (I). The
CC method is simple and eliminates time-consuming in vitro processing and
CC operations such as dissolution of inclusion bodies, reduction and

SQ Sequence 131 AA;
Query Match 100.0%; Score 81; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QKRAAYDQYGHAAFE 15
Db 84 QKRAAYDQYGHAAFE 98
RESULT 16
AAU17588
ID AAU17588 standard; protein; 340 AA.
AC AAU17588;
XX
DT 07-NOV-2001 (first entry)
XX
DE Novel signal transduction pathway protein, Seq ID 1153.
XX
KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
immune system disorder; rheumatoid arthritis; inflammatory condition;
organ transplant rejection; infection; hepatitis C; blood disorder;
sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
reproductive system; gastrointestinal; liver disorder; AIDS;
acquired immune deficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200154733-A1.
XX
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001312.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226661P.
PR 22-AUG-2000; 2000US-0226668P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
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PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI: 2001-465460/50.
DR N-PSDB; AAS27505.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX
PS Claim 1; SEQ ID NO 1153; 880pp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
CC AAU17683 represent novel signal transduction pathway protein, amino acid
CC sequences of the invention
XX

Query Match 100.0%; Score 81; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. NO. 3.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OKRAAYDOYGHAAFE 15

Db |||||||||||||
25 OKRAAYDOYGHAAFE 39
RESULT 17
ADB94296
ID ADB94296 standard; protein; 340 AA.
XX AC ADB94296;
XX 04-DEC-2003 (first entry)
XX Human novel protein #530.
XX human; autoimmune disease; Parkinson's disease; silicosis;
KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
KW immunosuppressive agent; adjuvant; enhance immune response;
KW higher affinity antibody induction;
KW increased serum immunoglobulin concentration.
XX OS Homo sapiens.
XX US2002168711-A1.
XX 14-NOV-2002.
XX 17-JAN-2001; 2001US-00764868.
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
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PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
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PR 14-AUG-2000; 2000US-0225757P.
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PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.

PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI; 2003-719985/68.
 DR N-PSDB; ADB93673.
 XX
 PT New isolated polypeptide useful for diagnosing and treating
 PT immunosuppressive conditions such as autoimmune disease and Parkinson's
 PT disease.
 XX
 PS Claim 11; SEQ ID NO 1153; 345pp; English.
 CC
 CC The invention relates to an isolated polypeptide. The polypeptide is
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition in a subject, by determining the presence or
 CC amount of expression of the polypeptide in a biological sample and
 CC diagnosing a pathological condition or a susceptibility to a pathological
 CC condition based on the presence or amount of expression of the
 CC polypeptide. The polypeptide is also useful for identifying a binding
 CC partner to the polypeptide, which involves contacting the polypeptide
 CC with a binding partner and determining whether the binding partner
 CC effects an activity of the polypeptide. The polypeptide or the nucleic
 CC acid encoding the polypeptide is useful for preventing, treating, or
 CC ameliorating a medical condition, which involves administering the
 CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
 CC is useful for diagnosing a pathological condition or a susceptibility to
 CC a pathological condition in a subject, which involves determining the
 CC presence or absence of a mutation in the nucleic acid, and diagnosing a
 CC pathological condition or susceptibility to a pathological condition
 CC based on the presence or absence of the mutation. The polypeptide, the
 CC nucleic acid and an antibody to the polypeptide are useful for treating
 CC autoimmune disease. Parkinson's disease, silicosis, gastrointestinal
 CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,
 CC the nucleic acid and the antibody are useful as immunosuppressive agents,
 CC as adjuvants to enhance immune responses, and as agents to induce higher
 CC affinity antibodies and increase serum immunoglobulin concentrations. The
 CC present sequence represents the amino acid sequence of a novel human
 CC protein. Note: The sequence data for this patent did not form part of the
 CC printed specification but was obtained in electronic format direct from
 CC USPTO at seqdata.uspto.gov/sequence.html?docID=20020168711.
 XX
 SQ Sequence 340 AA;
 Query Match 100.0%; Score 81; DB 7; Length 340;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 Db 25 QKRAAYDQYGHAAFE 39
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 RESULT 18
 AAU17587
 ID AAU17587 standard; protein; 341 AA.
 XX
 AC AAU17587;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Novel signal transduction pathway protein, Seq ID 1152.
 XX
 XX Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
 KW

immune system disorder; rheumatoid arthritis; inflammatory condition;
 organ transplant rejection; infection; hepatitis C; blood disorder;
 sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
 neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
 cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
 reproductive system; gastrointestinal; liver disorder; AIDS;
 acquired immune deficiency syndrome.
 OS Homo sapiens.
 XX
 XX WO200154733-A1.
 XX
 PD 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US001312.
 PF
 PF 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
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 PR 28-JUN-2000; 2000US-0214886P.
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PR 14-SEP-2000; 2000US-0232401P.
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PR 20-OCT-2000; 2000US-0241787P.
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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465460/50.
XX N-ESDB; AAS27504.
XX
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
XX prognosing disorders related to the proteins, including cancers, immune
XX disorders and neuronal disorders.
XX
XX Claim 1; SEQ ID NO 1152; 880pp; English.
XX
XX The invention relates to novel isolated polypeptides (I), and
XX polynucleotides (II). (I), (II) and the antibody to (I) are useful for
XX diagnosing, preventing and treating diseases including immune system
XX disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
XX disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
XX transplant rejections and graft versus host disease, infectious diseases
XX (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
XX other blood-related disorders (sickle cell anaemia), myeloproliferative
XX disorders, primary haematopoietic disorders, hyperproliferative disorders
XX (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
XX Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (e.g.
XX Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
XX glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
XX respiratory disorders, dermatological disorders, in wound healing,
XX epithelial cell proliferation, endocrine disorders (e.g. Addison's
XX disease), reproductive system disorders, gastrointestinal disorder
XX (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
XX B-cell responsiveness to pathogens, activators of T-cells, to induce
XX higher affinity antibodies, and as a means to induce tumour proliferation
XX in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
XX AAU17683 represent novel signal transduction pathway protein, amino acid
XX sequences of the invention
XX
XX
Query Match 100.0%; Score 81; DB 4; Length 341;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
DB 26 QKRAAYDQYGHAAFE 40
RESULT 19
ADB94295
ID ADB94295 standard; protein; 341 AA.
XX
XX ADB94295;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human novel protein #529.
XX
XX human; autoimmune disease; Parkinson's disease; silicosis;
XX gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
XX immunosuppressive agent; adjuvant; enhance immune response;
XX higher affinity antibody induction;
XX increased serum immunoglobulin concentration.
XX
XX Homo sapiens.
XX
XX US2002168711-A1.
PN
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XX PS Claim 2; SEQ ID NO 582; 1205pp; French.

XX CC The invention relates to the isolation of genes and their encoded

XX CC proteins from Photorhabdus luminescens. The isolated sequences are

XX CC sources of probes and primers for detecting the genome of P. luminescens

XX CC and related species; to study polymorphisms; for gene analysis and for

XX CC detection/amplification of the genes. Antibodies (Ab) raised against the

XX CC polypeptides encoded by the genes are used for detection/identification

XX CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that

XX CC carry a gene-containing vector are used to select compounds that

XX CC modulate, regulate, induce or inhibit expression of the genes in plants,

XX CC animals or microorganisms other than P. luminescens and are able to alter

XX CC response or sensitivity to toxins and antibiotics produced by P.

XX CC luminescens. Cells transformed to express the genes are useful for

XX CC recombinant production of the proteins, particularly toxins and

XX CC antibacterials useful as insecticides, bactericides and fungicides. The

XX CC genes, proteins, vectors containing the genes and Ab are also useful

XX CC therapeutically (to treat microbial infection by bacteria or fungi that

XX CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as

XX CC biopesticides. Other uses of the genes and the proteins are as virulence

XX CC factors and for identifying targets of human diseases for which P.

XX CC luminescens is a model (particularly plague and whooping cough). This

XX CC sequence represents one of the isolated P. luminescens proteins

XX SQ Sequence 373 AA;

Query Match 100.0%; Score 81; DB 6; Length 373;

Best Local Similarity 100.0%; Pred. No. 4.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

DB 61 QKRAAYDQYGHAAFE 75

RESULT 21

ADNR89339

ID ADNR89339 standard; protein; 376 AA.

XX AC ADNR89339;

XX DT 18-NOV-2004 (first entry)

XX DE E. coli protein-folding-related factor, DnaJ.

XX KW PFRF; protein-folding-related factor; chaperone; GroES; GroEL; DnaK;

XX KW DnaJ; GrpE; gene function; cell-free synthesis;

XX KW recombinant protein production; therapeutic protein.

XX OS Escherichia coli.

XX PN WO2004072107-A1.

XX PD 26-AUG-2004.

XX PF 13-FEB-2004; 2004WO-KR000302.

XX PR 15-FEB-2003; 2003KR-00009628.

XX PA (DREA-) DREAMBIOGEN CO LTD.

XX PI Kang SH, Choi WJ, Kim HJ, Jun SY, Lee KY;

XX DR WPI; 2004-616042/59.

XX PT Producing soluble proteins using transformed genes encoding protein-

XX PT folding-related factors in a cell-free protein synthesis system, useful

XX PT in therapeutic, industrial and research purposes.

XX PS Example 1; SEQ ID NO 4; 58pp; English.

XX CC The invention relates to producing soluble protein. The method involves

CC preparing cells transformed by genes encoding protein-folding-related

CC factors (PFRF), so that the transformed cells can express enhanced levels

CC of the PFRFs, over-expressing the factors and preparing a cell extract

CC for a cell-free protein synthesis system from the transformed cells, and

CC producing a high level of soluble protein in the synthesis system

CC containing the extract containing the factors. The folding-related factor

CC in producing a soluble protein is one or more in number, and/or is a

CC chaperone that is GroES/GroEL chaperone family or DnaK/DnaJ/GrpE

CC chaperone family. The cell extract is prepared from one or more

CC transformed cells. The protein is alpha, beta, gamma-interferon, lipase,

CC erythropoietin, cytokines, interleukins, granulocyte-colony stimulating

CC factor, granulocyte macrophage-colony stimulating factor, transforming

CC growth factors, thrombopoietin, or tissue plasminogen activator. The

CC methods and compositions of the present invention are useful for

CC producing soluble proteins applicable to therapeutic, industrial and

CC research purposes, in particular for assaying functions of newly

CC discovered genes. The present sequence represents the amino acid sequence

CC of an E. coli DnaJ, a protein-folding-related factor.

XX SQ Sequence 376 AA;

Query Match 100.0%; Score 81; DB 8; Length 376;

Best Local Similarity 100.0%; Pred. No. 4.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

DB 61 QKRAAYDQYGHAAFE 75

RESULT 22

ADNR18036

ID ADNR18036 standard; protein; 376 AA.

XX AC ADNR18036;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #689.

XX KW Recombinant DNA construct; transformed plant; improved plant property;

XX KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

XX KW pathogen tolerance; pest tolerance; plant disease resistance;

XX KW cell cycle pathway modification; plant growth regulator;

XX KW homologous recombination; seed oil yield; protein yield; carbohydrate;

XX KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

XX KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.

XX PA (HINK/) HINKLE G J.

XX PA (SLAT/) SLATER S C.

XX PA (CHEN/) CHEN X.

XX PA (GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX DR WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide

XX PT for expression of a polynucleotide encoding a polypeptide from a

XX PT microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 689; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 376 AA;

Query Match 100.0%; Score 81; DB 8; Length 376;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
|||||
DB 61 QKRAAYDQYGHAAFE 75

RESULT 23

ADN17733

ID ADN17733 standard; protein; 378 AA.

AC ADN17733;

XX 02-DEC-2004 (first entry)

DE Bacterial polypeptide #386.

XX Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

DR WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

PS Claim 1; SEQ ID NO 386; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 378 AA;

Query Match 100.0%; Score 81; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

DB 61 QKRAAYDQYGHAAFE 75

RESULT 24

ADS42875

ID ADS42875 standard; protein; 378 AA.

XX ADS42875;

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #21305.

XX Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 21305; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 378 AA;

Query Match 100.0%; Score 81; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. NO. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75
|||||

RESULT 25
ADF05627
ID ADF05627 standard; protein; 380 AA.
XX
XX ADF05627;
AC
XX 12-FEB-2004 (first entry)
DT
XX Bacterial polypeptide #1740.
DE
XX
XX Proteus mirabilis infection; bacterial infection; antibacterial;
KW immunostimulant.
KW
XX Proteus mirabilis.
OS
XX US6605709-B1.
PN
XX 12-AUG-2003.
PD
XX 05-APR-2000; 2000US-00543681.
PF
XX 09-APR-1999; 99US-0128706P.
PR

XX (GENO-) GENOME THERAPEUTICS CORP.
PA Breton GL;
XX
XX WPI; 2003-895291/82.
DR N-PSDB; ADF01455.
DR
XX New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX
XX Disclosure; SEQ ID NO 5912; 870pp; English.
XX
XX The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides. Methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX
XX SQ Sequence 380 AA;

Query Match 100.0%; Score 81; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. NO. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 63 QKRAAYDQYGHAAFE 77
|||||

RESULT 26
ABO62494
ID ABO62494 standard; protein; 380 AA.
XX
XX ABO62494;
AC
XX 29-JUL-2004 (first entry)
DT
XX Klebsiella pneumoniae polypeptide seqid 9011.
DE
XX
XX Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
KW
XX Klebsiella pneumoniae.
OS
XX US6610836-B1.
PN
XX 26-AUG-2003.
PD
XX 27-JAN-2000; 2000US-00489039.
PF
XX 29-JAN-1999; 99US-0117747P.
PR
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX Breton GL, Osborne M;
PI
XX WPI; 2003-895346/82.
DR N-PSDB; ACH96045.
DR
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
PT
XX Disclosure; SEQ ID NO 9011; 932pp; English.
PS

XX The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 81; DB 7; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
 DB 64 OKRAAYDQYGHAAFE 78

RESULT 27
 AAB11395
 ID AAB11395 standard; protein; 399 AA.
 AC AAB11395;
 XX
 XX 22-FEB-2001 (first entry)
 DT
 XX
 XX E. coli expression plasmid pUBS20-pIN-dnaJ encoded protein.
 DE
 XX
 XX Eukaryotic protein; protease; interferon; antibody; hormone;
 KW disulfide bridge.
 KM
 XX Escherichia coli.
 OS Synthetic.
 OS
 XX
 XX EP1048732-A1.
 PN
 XX
 XX 02-NOV-2000.
 PD
 XX
 XX 26-APR-1999; 99EP-00107412.
 PF
 XX
 XX 26-APR-1999; 99EP-00107412.
 PR
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA
 XX
 XX WPI; 2000-674185/66.
 DR N-PSDB; AAC66071.
 DR
 XX Preparation of water-soluble eukaryotic polypeptides with disulfide
 PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
 PT presence of arginine or amide compound.
 PT
 XX
 XX Example 2; Page 13-15; 40pp; German.
 PS
 XX
 XX This invention describes a novel preparation of a water-soluble,
 CC naturally occurring eukaryotic polypeptide containing two or more
 CC cysteine units bound via a disulfide bridge which comprises cultivation
 CC of prokaryotic cells in the presence of arginine or an amide compound.
 CC The method is useful for the preparation of eukaryotic proteins e.g.
 CC proteases, interferons, protein hormones, antibodies or antibody
 CC fragments (e.g. a single chain Fv fragment that binds to thyroid
 CC stimulating hormone). It is especially useful for preparing proteins with
 CC more than five disulfide bridges, e.g. recombinant plasminogen activator
 CC (rPA). The technique is simple and does not require in vitro after-
 CC treatment, such as the removal of inclusion bodies, reduction or
 CC naturalization
 CC
 XX Sequence 399 AA;

Query Match 100.0%; Score 81; DB 3; Length 399;
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
 DB 84 OKRAAYDQYGHAAFE 98

RESULT 28
 AAB74196
 ID AAB74196 standard; protein; 399 AA.
 XX
 XX AAB74196;
 AC
 XX 29-MAY-2001 (first entry)
 DT
 XX
 XX OmpA-DnaJ fusion protein.
 DE
 XX
 XX Molecular chaperone; OmpA signal sequence; DnaJ.
 KW
 XX
 XX Unidentified.
 OS
 XX EP1077262-A1.
 PN
 XX
 XX 21-FEB-2001.
 PD
 XX
 XX 24-JUL-2000; 2000EP-00115839.
 PF
 XX
 XX 29-JUL-1999; 99EP-00114811.
 PR
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA
 XX
 XX Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
 PI
 XX WPI: 2001-246712/26.
 DR N-PSDB; AAF77803.
 DR
 XX Producing naturally folded eukaryotic proteins e.g. antibodies,
 PT interferon, hormones or proteases that contain two or several cysteines
 PT linked by disulfide bridges comprises co-expression of a molecular
 PT chaperone.
 PT
 XX Disclosure; Page 11-12; 35pp; English.
 PS
 XX The present invention relates to a method for production of a naturally
 CC folded eukaryotic protein containing two or more cysteines linked by
 CC disulfide bridges. The method comprises co-expression and secretion into
 CC the periplasm of a molecular chaperone via an expression vector coding
 CC for the chaperone. The expression vector also encodes a signal sequence.
 CC The method is useful for producing a naturally folded eukaryotic protein
 CC such as an antibody, antibody fragment, interferon, protein hormone or a
 CC protease containing two or several cysteines linked by disulfide bridges.
 CC The present sequence is a fusion protein composed of the OmpA signal
 CC sequence and DnaJ. This sequence was used in the method of the present
 CC invention
 CC
 XX Sequence 399 AA;

Query Match 100.0%; Score 81; DB 4; Length 399;
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
 DB 84 OKRAAYDQYGHAAFE 98

RESULT 29
 AAB70766
 ID AAB70766 standard; protein; 399 AA.
 XX
 XX AAB70766;
 AC
 XX 18-MAY-2001 (first entry)
 DT
 XX

DE Expression plasmid pUBS520-pIN-dnaJ protein.
 XX Chaperone protein; periplasm; antibody production; protein production;
 KW interferon production; protease production.
 XX Escherichia coli.
 OS Synthetic.
 XX EP1077263-A1.
 XX 21-FEB-2001.
 XX 29-JUL-1999; 99EP-00114811.
 XX 29-JUL-1999; 99EP-00114811.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX WPI; 2001-204356/21.
 DR N-PSDB; AAP61190.
 XX Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by
 PT simultaneous expression of a chaperone protein, allows simple recovery
 PT from periplasm or medium.
 XX Disclosure; Page 11-13; 36pp; German.
 XX This invention describes a novel method for preparing a naturally folded
 CC eukaryotic polypeptide (I) that contains two or more disulfide-bridged
 CC Cys residues by culturing prokaryotic cells that contain an expression
 CC vector for (I) including a prokaryotic signal sequence at its N-terminus
 CC and a nucleic acid (II) that secretes a chaperone protein (III) into the
 CC periplasm. (I) is secreted into the periplasm or medium; the signal
 CC peptide is then cleaved and (I) isolated from the periplasm or medium.
 CC The method is used for production of antibody, interferon, protein
 CC hormone or protease. Expression of (III) increases the yield of (I). The
 CC method is simple and eliminates time-consuming in vitro processing
 CC operations such as dissolution of inclusion bodies, reduction and
 CC refolding. (III) protects (I) against agglomeration and promotes their
 CC natural conformation
 XX Sequence 399 AA;
 SQ
 Query Match 100.0%; Score 81; DB 4; Length 399;
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 OKRAAYDQYGHAAFE 15
 DB 84 QKRAAYDQYGHAAFE 98
 RESULT 30
 AA72017
 ID AA72017 standard; protein; 399 AA.
 AC AA72017;
 XX 28-MAR-2001 (first entry)
 DT E. coli OmpA-DnaJ fusion protein encoded by pUBS520-pIN-dnaJ.
 DE
 XX Secreted protein; chaperone; interferon; protease; hormone;
 KW fusion protein; naturally folded protein; lac-ipp promoter; DnaJ;
 KW heat shock protein; HSP; outer membrane protein A; OmpA.
 XX Escherichia coli.
 OS
 XX EP1054063-A2.
 PN 22-NOV-2000.
 XX 19-APR-2000; 2000EP-00108505.
 PF

XX 26-APR-1999; 99EP-00107412.
 PR (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
 PI WPI; 2001-033777/05.
 DR N-ESDB; AAD02209.
 XX Producing water-soluble, naturally folded, and secreted eukaryotic
 XX polypeptide, involves culturing prokaryotic cells containing an
 PT expression vector encoding the polypeptide in the presence of arginine or
 PT a specific compound.
 XX Example 2; Page 13-15; 35pp; English.
 XX The patent discloses a method for the production of a water-soluble,
 CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.
 CC The method involves culturing the prokaryotic cells, containing an
 CC expression vector encoding the desired protein and the prokaryotic signal
 CC sequence, in the presence of an additive, e.g., L-arginine. The signal
 CC sequence mediates the secretion of the desired protein into the
 CC periplasm, where folding of the protein takes place. The prokaryotic cell
 CC also contains an expression vector encoding a molecular chaperone, e.g.,
 CC DnaJ and heat shock protein 25 (HSP25). The simultaneous co-
 CC overexpression and co-secretion of molecular chaperones in the periplasm
 CC improves the yield of functionally folded protein. The above method
 CC recombinantly produces a high yield of eukaryotic secreted proteins in
 CC prokaryotes. The method is useful for producing eukaryotic proteins such
 CC as an antibody, antibody fragment, interferon, protein hormone or a
 CC protease. The present sequence is an Escherichia coli outer membrane
 CC protein A (OmpA) signal sequence-dnaJ fusion protein encoded by pUBS520-
 CC pIN-dnaJ. The plasmid, pUBS520-pIN-dnaJ, also contains the lac-ipp
 CC promoter and the ipp terminator. The periplasmic co-secretion of DnaJ
 CC facilitates the folding of the desired secreted protein
 XX Sequence 399 AA;
 SQ
 Query Match 100.0%; Score 81; DB 4; Length 399;
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 OKRAAYDQYGHAAFE 15
 DB 84 QKRAAYDQYGHAAFE 98
 RESULT 31
 AAU02077
 ID AAU02077 standard; protein; 459 AA.
 XX AAU02077;
 AC AAU02077;
 XX 07-SEP-2001 (first entry)
 DT Synthetic multi-target autoantigen Y-RAPb.
 DE
 XX Y-RAPa; immunogenic epitope cluster; IEC; autoantigen; shCollagen/RA;
 KW shagrecan/RA; shGLP/RA; shHSP/RA; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis;
 KW insulin-dependent diabetes mellitus; myasthenia gravis; uveitis;
 KW autoimmune hepatitis; thyroiditis; insulinitis; orchitis;
 KW idiopathic thrombocytopenic purpura; inflammatory disease;
 KW Crohn's disease; ulcerative colitis; shMultiTAG.
 XX Synthetic.
 OS Homo sapiens.
 OS Escherichia coli.
 OS Mycobacterium tuberculosis.
 XX Key Location/Qualifiers
 FT Misc-difference 455

FT /label= OTHER
FT /note= "Other= STOP"
FT Misc-difference 457
FT /label= OTHER
FT /note= "Other= STOP"
XX
XX WO200131037-A2.
XX
XX PN
XX PD 03-MAY-2001.
XX
XX PF 26-OCT-2000; 2000WO-IL000688.
XX
XX PR 27-OCT-1999; 99IL-00132611.
XX
XX PA (YEDA) YEDA RES & DEV CO LTD.
XX
XX PI Ben-Nun A, Kerlero De Rosbo N, Sappier GP;
XX
XX DR WPI; 2001-300515/31.
XX
XX DR N-PSDB; AAS04838.
XX
XX PT Novel synthetic human target autoantigen gene useful for treating
PT autoimmune diseases such as multiple sclerosis, insulin-dependent
PT diabetes mellitus, rheumatoid arthritis, myasthenia gravis, and uveitis.
XX
XX PS Claim 182; Fig 57; 182pp; English.
XX
XX CC The sequence represents synthetic human multi-target autoantigen
CC (shMULTITAG) Y-RAPA consisting of regions encoding shCollagen/RA,
CC shAggrecan/RA, shGLP/RA and shHSP/RA. The synthetic human target
CC autoantigen genes of the invention comprise sequences coding for at least
CC 2 IECs of autoantigen(s) related to a specific autoimmune disease. The
CC synthetic human target autoantigen genes are useful for treating
CC autoimmune diseases such as multiple sclerosis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, myasthenia gravis, uveitis,
CC autoimmune hepatitis, thyroiditis, insulinitis, orchitis, idiopathic
CC thrombocytopenic purpura, and inflammatory diseases (Crohn's disease,
CC ulcerative colitis). The synthetic human target autoantigen genes are
CC also useful for diagnosis and/or monitoring the progression of the
CC autoimmune disease
XX
XX SQ Sequence 459 AA;
Query Match 100.0%; Score 81; DB 4; Length 459;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
|||||
Db 440 QKRAAYDQYGHAAFE 454
RESULT 32
ABG17771
ID ABG17771 standard; protein; 476 AA.
XX
XX AC ABG17771;
XX
XX DT 18-FEB-2002 (first entry)
XX
XX DE Novel human diagnostic protein #17762.
XX
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200175067-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US008631.
XX
XX

PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Drmanac RT, Liu C, Tang YT;
XX
XX DR WPI; 2001-639362/73.
XX
XX DR N-PSDB; AAS81958.
XX
XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX PS Claim 20; SEQ ID NO 48130; 103pp; English.
XX
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 476 AA;
Query Match 100.0%; Score 81; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
|||||
Db 81 QKRAAYDQYGHAAFE 95
RESULT 33
ADS21615
ID ADS21615 standard; protein; 365 AA.
XX
XX AC ADS21615;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Bacterial polypeptide #10648.
XX
XX KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX
XX KW Bacterial polypeptide.
XX
XX OS Bacteria.
XX
XX PN US2003233675-A1.
XX
XX PD 18-DEC-2003.

```
XX PF 20-FEB-2003; 2003US-00369493.
XX PR
XX PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX DR WPI; 2004-061375/06.
XX PT New recombinant DNA construct comprising a promoter positioned to provide
XX PT for expression of a polynucleotide encoding a polypeptide from a
XX PT microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 10648; 122pp; English.
XX CC The invention relates to a recombinant DNA construct comprising a
XX CC promoter functional in a plant cell, where the promoter is positioned to
XX CC provide for expression of a polynucleotide encoding a polypeptide from a
XX CC microbial source. The invention also relates to a transformed plant
XX CC comprising the recombinant DNA construct and a method of producing a
XX CC transformed plant having an improved property. The plant is a crop plant
XX CC such as maize or soybean. The method of producing a transformed plant
XX CC having an improved property comprises transforming a plant with the
XX CC recombinant DNA construct and growing the transformed plant, where the
XX CC polynucleotide or polypeptide is useful for improving plant properties.
XX CC The recombinant DNA construct is useful for producing plants with
XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,
XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX CC increased resistance to plant disease, better growth rate by modification
XX CC of the cell cycle pathway with plant growth regulators, increased rate of
XX CC homologous recombination, modified seed oil or protein yield and/or
XX CC content, improved yield by modification of carbohydrate, nitrogen or
XX CC phosphorus use and/or uptake, by modification of photosynthesis or by
XX CC providing improved plant growth and development under at least one stress
XX CC condition, improved lignin production or improved galactomannan
XX CC production. This sequence represents a bacterial polypeptide used in the
XX CC scope of the invention. Note: The sequence data for this patent did not
XX CC form part of the printed specification but was obtained in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 365 AA;
Query Match 91.4%; Score 74; DB 8; Length 365;
Best Local Similarity 86.7%; Pred. No. 7.9e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 2;
QY 1 OKRAAYDQYGHAAFE 15
Db 56 OKRAAYDRYGHAAFA 70
RESULT 34
ABP08077
ID ABP08077 standard; protein; 344 AA.
XX AC
XX AC ABP08077;
XX DT 07-MAR-2003 (first entry)
XX DE N. gonorrhoeae amino acid sequence SEQ ID 8284.
XX KW Antibacterial; infection; vaccine; gene therapy.
XX OS Neisseria gonorrhoeae.
XX PN WO200279243-A2.
XX PI
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PD 10-OCT-2002.
XX 12-FEB-2002; 2002WO-IB002069.
XX PF
XX PR 12-FEB-2001; 2001GB-00003424.
XX PA (CHIR-) CHIRON SPA.
XX PI Fontana MR, Pizza M, Maignani V, Monaci E;
XX DR WPI; 2003-058415/05.
XX DR N-PSDB; ABZ41847.
XX PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a
XX PT medicament for treating or preventing N. gonorrhoeae infection.
XX PS Disclosure; Page 792; 815pp; English.
XX CC The present invention relates to proteins from Neisseria gonorrhoeae.
XX CC Also disclosed are the nucleic acid molecules encoding the proteins and
XX CC antibodies that specifically bind to the proteins. The composition
XX CC comprising the protein, nucleic acid or antibody is useful for the
XX CC manufacture of a medicament for treating or preventing N. gonorrhoeae
XX CC infection, this may be in the form of a vaccine or gene therapy.
XX CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
XX CC molecules of the invention
XX SQ Sequence 344 AA;
Query Match 90.1%; Score 73; DB 6; Length 344;
Best Local Similarity 86.7%; Pred. No. 0.00011;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 OKRAAYDQYGHAAFE 15
Db 32 EKRAAYDQYGHAAFE 46
RESULT 35
ADS23054
ID ADS23054 standard; protein; 376 AA.
XX AC
XX AC ADS23054;
XX DT 02-DEC-2004 (first entry)
XX DE
XX DE Bacterial polypeptide #12087.
XX KW Recombinant DNA construct; transformed plant; improved plant property;
XX KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX KW pathogen tolerance; pest tolerance; plant disease resistance;
XX KW cell cycle pathway modification; plant growth regulator;
XX KW homologous recombination; seed oil yield; protein yield; carbohydrate;
XX KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX KW bacterial polypeptide.
XX OS Bacteria.
XX PN US2003233675-A1.
XX PD 18-DEC-2003.
XX XX 20-FEB-2003; 2003US-00369493.
XX PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
```

XX WPI; 2004-061375/06.
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 12087; 122pp; English.
 XX
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. Improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 376 AA;

Query Match 90.1%; Score 73; DB 8; Length 376;
 Best Local Similarity 86.7%; Pred. No. 0.00012;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
 :|||||:|||||
 Db 60 QKRAAYDRFGHAAPE 74

RESULT 36
 AAR95446
 ID AAR95446 standard; peptide; 15 AA.

XX AAR95446;
 XX
 DT 01-JUL-1996 (first entry)

XX RA susceptibility sequence peptide #2.

XX Rheumatoid arthritis; RA; dnaJ; E.coli; heat shock protein; antibody;
 KW arthritogenic peptide; RA-beggn bacteria; Escherichia; Lactococcus;
 KW Klebsiella; Proteus; therapy.

XX Synthetic.

XX Key Location/Qualifiers
 XX Region 1..5
 FT /note= "rheumatoid arthritis susceptibility sequence"
 FT Misc-difference 1 /note= "Q1D"
 FT Misc-difference 2 /note= "K2E"

XX W09531984-A1.

XX 30-NOV-1995.

XX

PF 24-APR-1995; 95WO-US004896.
 XX
 PR 20-MAY-1994; 94US-00246988.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Carson DA, Salvatore A;
 XX
 XX WPI; 1996-020344/02.

XX Treatment of rheumatoid arthritis - by limiting exposure of immune system
 PT to arthritogenic peptide(s).

XX Example 3; Page 36; 52pp; English.

XX AAR95445 and AAR95446 represent rheumatoid arthritis (RA) susceptibility
 CC sequence (see AAR95443 and AAR95444) containing peptides. This sequence
 CC corresponds to a region of dnaJ. These sequences are present on
 CC arthritogenic proteins and are targeted in this invention as antibody
 CC recognition sites. The anti-arthritogenic peptide antibodies that are
 CC developed can then be administered to a patient who has RA or who is
 CC predisposed to develop RA, to reduce the exposure to arthritogenic
 CC peptides. The antibodies are produced and administered in milk. An
 CC alternative treatment method comprises the administration of a non-
 CC adsorbable antibiotic, together with a RA-beggn bacteria (selected from
 CC the genera Escherichia, Lactococcus, Klebsiella and Proteus), to the
 CC patient who has RA (or a predisposition to it). Candidates for either of
 CC these methods can be screened by detecting an in-vitro cellular immune
 CC response to an arthritogenic peptide. The method of the invention allows
 CC for the reduction of sensitisation to microbial arthritogenic peptides
 CC (such as dnaJ). It also limits the exposure of the systemic immune system
 CC of humans to RA arthritogenic peptides present in the gastrointestinal
 CC tract
 XX
 SQ Sequence 15 AA;

Query Match 88.9%; Score 72; DB 2; Length 15;
 Best Local Similarity 92.9%; Pred. No. 5.5e-06;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAPE 15
 :|||||:|||||
 Db 2 ERAAYDQYGHAAPE 15

RESULT 37
 AAR25796
 ID AAR25796 standard; peptide; 15 AA.

XX AAR25796;

DT 06-APR-1998 (first entry)

XX Peptide dnaJpV which protects against arthritogenic peptides.

XX dnaJ protein; dnaJp1; adult rheumatoid arthritis; vaccine;
 KW arthritogenic peptide; autoimmune disease; systemic immune system;
 KW anti-dnaJp1 antibody; passive immunisation;
 KW rheumatoid arthritis-susceptibility detection.

XX Synthetic.
 OS Escherichia coli.

XX Key Location/Qualifiers
 XX Region 1..5
 FT /note= "wild type Gln substituted with Asp"
 FT Misc-difference 1 /label= Q1D
 FT Misc-difference 2 /note= "wild type Lys substituted with Glu"

XX W09734002-A1.

XX

XX 25-SEP-2001; 2001US-0325499P.
 PR 11-DEC-2001; 2001US-0339284P.
 XX (REGC) UNIV CALIFORNIA.
 PA Albani S, Martins A;
 XX WPI; 2003-430097/40.
 DR
 XX Modulating an immune response in a subject having an immune-related
 PT disorder, e.g. arthritis by administering an antigen-specific epitope and
 PT a cytokine or an agent that effects cytokine activity or expression.
 XX
 PS Disclosure; Page 9; 41pp; English.
 XX
 CC The invention relates to a novel method for modulating an immune response
 CC in a subject having an immune-related disorder. The method comprises: (a)
 CC administering an antigen-specific epitope, where administration provides
 CC epitope-specific T cell immune modulation; and (b) administering a
 CC cytokine, an agent that effects cytokine activity or expression, or an
 CC anticytokine therapy. The method of the invention has antiarthritic,
 CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,
 CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
 CC ulcer, antianaemic, cardiac, respiratory general, antiallergic,
 CC dermatological, and antipsoiratic activity. The method is useful for
 CC modulating an immune response in a subject having an immune-related
 CC disorder. The present sequence is used in the exemplification of the
 CC invention
 XX
 SQ Sequence 15 AA;
 Query Match 88.9%; Score 72; DB 6; Length 15;
 Best Local Similarity 92.9%; Pred. No. 5.5e-06;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 KRAAYDQYGHAAFE 15
 Db :|||||:|||||
 2 ERAAYDQYGHAAFE 15
 RESULT 40
 ADN25412
 ID ADN25412 standard; protein; 382 AA.
 AC
 XX ADN25412;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #8065.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 XX
 XX 18-DEC-2003.
 XX
 XX 20-FEB-2003; 2003US-00369493.
 XX
 XX 21-FEB-2002; 2002US-0360039P.
 XX
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLATY/) SLATER S C.
 PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 DR
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 8065; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 382 AA;
 Query Match 85.2%; Score 69; DB 8; Length 382;
 Best Local Similarity 85.7%; Pred. No. 0.00067;
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 KRAAYDQYGHAAFE 15
 Db :|||||:|||||
 62 KRAAYDQYGHAAFE 75
 RESULT 41
 ADS43419
 ID ADS43419 standard; protein; 384 AA.
 XX
 XX ADS43419;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #21849.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 XX
 XX 18-DEC-2003.
 XX
 XX 20-FEB-2003; 2003US-00369493.

XX PN US2003233675-A1.
 XX KW 18-DEC-2003.
 PD KW
 XX PF 20-FEB-2003; 2003US-00369493.
 XX PF
 XX PR 21-FEB-2002; 2002US-0360039P.
 XX PR
 XX PA (CAOY/) CAO Y.
 XX PA (HINK/) HINKLE G J.
 XX PA (SLAT/) SLATER S C.
 XX PA (CHEN/) CHEN X.
 XX PA (GOLD/) GOLDMAN B S.
 XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 7330; 122pp; English.
 XX
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. Improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 XX SQ Sequence 379 AA;
 Query Match 82.7%; Score 67; DB 8; Length 379;
 Best Local Similarity 80.0%; Pred. No. 0.0015;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 Db ||||| :
 61 QKRAAYDQYGHAGVD 75
 RESULT 44
 ADN21920
 ID ADN21920 standard; protein; 380 AA.
 XX
 AC ADN21920;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 XX Bacterial polypeptide #4573.
 DE
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 AC

KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 XX OS
 XX PN US2003233675-A1.
 XX PN
 XX PD 18-DEC-2003.
 XX PD
 XX PF 20-FEB-2003; 2003US-00369493.
 XX PF
 XX PR 21-FEB-2002; 2002US-0360039P.
 XX PR
 XX PA (CAOY/) CAO Y.
 XX PA (HINK/) HINKLE G J.
 XX PA (SLAT/) SLATER S C.
 XX PA (CHEN/) CHEN X.
 XX PA (GOLD/) GOLDMAN B S.
 XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 4573; 122pp; English.
 XX
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. Improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 XX SQ Sequence 380 AA;
 Query Match 82.7%; Score 67; DB 8; Length 380;
 Best Local Similarity 80.0%; Pred. No. 0.0015;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 Db ||||| :
 61 QKRAAYDQYGHAGVD 75
 RESULT 45
 AAR95445
 ID AAR95445 standard; peptide; 14 AA.
 XX
 AC AAR95445;

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XX DT 01-JUL-1996 (first entry)
XX RA susceptibility sequence peptide #1.
XX Rheumatoid arthritis; RA; dnaJ; E.coli; heat shock protein; antibody;
KW arthritogenic peptide; RA-beggn bacteria; Escherichia; Lactococcus;
KW Klebsiella; Proteus; therapy.
XX Escherichia coli.
XX OS
XX FH Key Location/Qualifiers
FT Region 1..5
FT /note= "rheumatoid arthritis susceptibility sequence"
XX WO9531984-A1.
XX PN
XX PD 30-NOV-1995.
XX PF 24-APR-1995; 95WO-US004896.
XX PR 20-MAY-1994; 94US-00246988.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Carson DA, Salvatore A;
XX WPI; 1996-020344/02.
XX DR
XX PT Treatment of rheumatoid arthritis - by limiting exposure of immune system
XX to arthritogenic peptide(s).
XX PS Example 3; Page 36; 52pp; English.
XX CC AAR95445 and AAR95446 represent rheumatoid arthritis (RA) susceptibility
XX sequence (see AAR95443 and AAR95444) containing peptides. This sequence
XX corresponds to a region of dnaJ. These sequences are present on
XX arthritogenic proteins and are targeted in this invention as antibody
XX recognition sites. The anti-arthritogenic peptide antibodies that are
XX developed can then be administered to a patient who has RA or who is
XX predisposed to develop RA, to reduce the exposure to arthritogenic
XX peptides. The antibodies are produced and administered in milk. An
XX alternative treatment method comprises the administration of a non-
XX adsorbable antibiotic, together with a RA-beggn bacteria (selected from
XX the genera Escherichia, Lactococcus, Klebsiella and Proteus), to the
XX patient who has RA (or a predisposition to it). Candidates for either of
XX these methods can be screened by detecting an in-vitro cellular immune
XX response to an arthritogenic peptide. The method of the invention allows
XX for the reduction of sensitisation to microbial arthritogenic peptides
XX (such as dnaJ). It also limits the exposure of the systemic immune system
XX of humans to RA arthritogenic peptides present in the gastrointestinal
XX tract
XX SQ Sequence 14 AA;
XX Query Match 79.6%; Score 64.5; DB 2; Length 14;
XX Best Local Similarity 93.3%; Pred. No. 0.00012;
XX Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX QY 1 OKRAAYDQYGHAAFE 15
XX Db 1 OKRAAYDQY-HAAFE 14
XX RESULT 46
XX ADN17394
XX ID ADN17394 standard; protein; 376 AA.
XX AC ADN17394;
XX XX
XX DT 02-DEC-2004 (first entry)
XX XX Bacterial polypeptide #47.

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XX XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.
XX OS Bacteria.
XX PN US2003233675-A1.
XX PD 18-DEC-2003.
XX PF 20-FEB-2003; 2003US-00369493.
XX PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX PT New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 47; 122pp; English.
XX CC The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 376 AA;
XX Query Match 77.8%; Score 63; DB 8; Length 376;
XX Best Local Similarity 73.3%; Pred. No. 0.008;
XX Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 OKRAAYDQYGHAAFE 15
XX Db 63 EKKLYDQYGHAAFE 77
XX RESULT 47
XX ADO25512

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PR 08-NOV-2002; 2002US-0425201P.
PR 12-MAR-2003; 2003US-0453914P.
PR 12-MAR-2003; 2003US-0454021P.
PR 12-MAR-2003; 2003US-0454128P.
PR 12-MAR-2003; 2003US-0454193P.
PR 13-MAR-2003; 2003US-0454215P.
PR 13-MAR-2003; 2003US-0454218P.
PR 13-MAR-2003; 2003US-0454487P.
PR 13-MAR-2003; 2003US-0454536P.
PR 14-MAR-2003; 2003US-0455010P.
PR 14-MAR-2003; 2003US-0455036P.
PR 14-MAR-2003; 2003US-0455054P.
PR 14-MAR-2003; 2003US-0455082P.
PR 17-MAR-2003; 2003US-0455191P.
PR 17-MAR-2003; 2003US-0455192P.
PR 17-MAR-2003; 2003US-0455334P.
PR 17-MAR-2003; 2003US-0455335P.
PR 17-MAR-2003; 2003US-0455343P.
XX (AFFI-) AFFINIUM PHARM INC.
XX
XX Edwards A, Dharamsi A, Vedadi M, Domagala M, Nethery K;
PI Mansoury K, Pinder B, Alam MZ, Ng I, Virag C, Houston S;
PI McDonald M, Buzadziya K;
XX
DR NPI; 2004-400642/37.
DR N-PSDB; ADO25509.
XX
XX Bacterial polypeptide composition useful for treating bacterial
PT infection, has isolated, recombinant bacterial polypeptide such as GTP-
PT binding protein Era from *Pseudomonas aeruginosa* or adenylosuccinate lyase
PT from *Enterococcus faecalis*.
XX
XX Claim 44; SEQ ID NO 185; 566pp; English.
XX
XX This invention relates to the identification of novel protein targets for
CC the development of antimicrobial drugs against pathogenic bacteria.
CC Specifically, it refers to recombinant proteins derived from
CC *Staphylococcus aureus*, *Helicobacter pylori*, *Streptococcus pneumoniae*,
CC *Escherichia coli*, *Enterococcus faecalis* or *Pseudomonas aeruginosa*. The
CC present invention describes providing a three-dimensional structure for
CC these crystallised proteins to identify a potential modulator for the
CC prevention or treatment of microbial diseases. Furthermore, contacting a
CC protein with a modulator can be useful for assaying protein activity and
CC hence its viability in drug composition or vaccine. Accordingly, such
CC compositions can be useful for treating bacterial infections, developing
CC antibacterial agents useful as food preservatives or treating food
CC products to eliminate potential pathogens. This polypeptide sequence is a
CC bacterial protein target of the invention.
XX
SQ Sequence 389 AA;
Query Match 77.8%; Score 63; DB 8; Length 389;
Best Local Similarity 91.7%; Pred. No. 0.0083; 0; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KRKAAYDQYQCHA 12
Db 61 QKKAAYDQYQCHA 72
:::|||||
:::|||||
RESULT 49
ADS24625
ID ADS24625 standard; protein; 374 AA.
XX
XX ADS24625;
AC
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Bacterial polypeptide #13658.
DE
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX US2003233675-A1.
PN 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
DR
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 13658; 122pp; English.
PS
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 374 AA;
Query Match 76.5%; Score 62; DB 8; Length 374;
Best Local Similarity 78.6%; Pred. No. 0.012;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 KRAAYDQYGHAAFE 15
Db 62 KRAAYDQYGHAGVD 75
|||||
|||||
RESULT 50
ABO78428
ID ABO78428 standard; protein; 381 AA.
XX

AC AB078428;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #10603.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-ESDB; ABD11999.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 27174; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnosis and
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences AB067826-
CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
SQ Sequence 381 AA;
Query Match 76.5%; Score 62; DB 7; Length 381;
Best Local Similarity 78.6%; Pred. No. 0.012;
Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 KRAAYDQYGHAAFE 15
Db ||||| :
66 KRAAYDQYGHAGVD 79
RESULT 51
ADN25797
ID ADN25797 standard; protein; 378 AA.
XX
AC ADN25797;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #8450.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 8450; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: the sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 378 AA;
Query Match 75.3%; Score 61; DB 8; Length 378;
Best Local Similarity 66.7%; Pred. No. 0.018;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 OKRAAYDQYGHAAFE 15
Db ||||| :
61 EKRAAYDQYGHAGVD 75
RESULT 52
ADN10662
ID ADN10662 standard; protein; 385 AA.
XX
AC ADN10662;
XX

DT 20-NOV-2003 (first entry)
XX Alloiococcus otitis antigenic protein SEQ ID NO:4398.
XX Alloiococcus otitis; antigenic protein; immunogenic; immunisation;
KW gene therapy; Gram-positive bacterium; infection.
XX Alloiococcus otitis.
XX WO2003048304-A2.
XX 12-JUN-2003.
XX 25-NOV-2002; 2002WO-US036123.
XX 29-NOV-2001; 2001US-0333777P.
PR 18-NOV-2002; 2002US-0426742P.
XX (AMHP) WYETH HOLDINGS CORP.
PA Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;
PI WPI: 2003-505284/47.
DR N-PSDB; ADB10665.
XX New Alloiococcus otitis polynucleotides and polypeptides, useful for
PT treating and diagnosing diseases, drug screening assays and monitoring of
PT effects during drug clinical trials.
XX Claim 33; SEQ ID NO 4398; 1019pp; English.
XX The present invention describes an isolated polynucleotide (I) of
CC Alloiococcus otitis genomic DNA, which encodes an antigenic protein.
CC Alloiococcus otitis is a Gram-positive bacterium. Also described: (1)
CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an
CC expression vector comprising the novel isolated polynucleotide (I), its
CC complement, degenerate variant or fragment; (3) a genetically engineered
CC host cell, transfected, transformed or infected with the vector of (2);
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
CC composition comprising the polypeptide, its complement, biological
CC equivalent or fragment, or the polynucleotide that is comprised in the
CC expression vector; (6) a pharmaceutical composition comprising the
CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
CC of the polypeptides of (1), their biological equivalent or fragment; (8)
CC immunising against Alloiococcus otitis by administering to a host the
CC immunogenic composition; (9) detecting and/or identifying Alloiococcus
CC otitis in the biological sample; (10) a kit comprising a container
CC containing the novel polynucleotide, its degenerate variant or fragment,
CC or the antibody of (4); and (11) producing a polypeptide by culturing the
CC genetically engineered host cell under conditions suitable to produce the
CC polypeptide from the culture. (I) can be used in gene therapy. The
CC polynucleotides, polypeptides, antibodies and compositions of the present
CC invention can be used for treating and diagnosing diseases, drug
CC screening assays and monitoring of effects during drug clinical trials.
CC The polynucleotides are useful for expressing and detecting Alloiococcus
CC otitis. The present sequence represents an Alloiococcus otitis
CC antigen protein from the present invention.
XX
SQ Sequence 385 AA;
Query Match 75.3%; Score 61; DB 6; Length 385;
Best Local Similarity 91.7%; Pred. No. 0.019;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 KRAAYDQYGHAA 13
DB 62 KRAAYDRYGHAA 73
|||||:|||||
RESULT 53
ADS26826
ID ADS26826 standard; protein; 375 AA.
XX

AC ADS26826;
XX
DT 02-DEC-2004 (first entry)
XX Bacterial polypeptide #15859.
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
OS
XX US2003233675-A1.
XX 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI: 2004-061375/06.
DR
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
PT
XX Claim 1; SEQ ID NO 15859; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 375 AA;
Query Match 74.1%; Score 60; DB 8; Length 375;
Best Local Similarity 78.6%; Pred. No. 0.028;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 KRAAYDQYGHAAFE 15
|||||:|||||

Db 62 KRAYDAHGAHAAFE 75

RESULT 54
ADS26454
ID ADS26454 standard; protein; 376 AA.
XX
AC ADS26454;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #15487.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
DR
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 15487; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC having an improved property comprising transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. Improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 376 AA;

Query Match 74.1%; Score 60; DB 8; Length 376;
Best Local Similarity 78.6%; Pred. No. 0.028; 2; Gaps 0;
Matches 11; Conservative 1; Mismatches 2; Indels 0;

QY 2 KRAAYDOYGHAAFE 15
||| :|||
Db 62 KRAYDAHGAHAAFE 75

RESULT 55

ADN26988
ID ADN26988 standard; protein; 358 AA.

XX
AC ADN26988;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #9641.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.

XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.

XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.

XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.

XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX
PS Claim 1; SEQ ID NO 9641; 122pp; English.

XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress

CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 358 AA;

Query Match 72.8%; Score 59; DB 8; Length 358;
Best Local Similarity 66.7%; Pred. No. 0.04;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQVGHAAPE 15
Db 46 EKRRYDQMGHSAFD 60
:||||| |||:|:|:

RESULT 56

AAG14804
ID AAG14804 standard; protein; 332 AA.

XX

AC AAG14804;

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 14804.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-00301439.

XX

25-FEB-1999; 99US-01218259.

PR

05-MAR-1999; 99US-0123180P.

PR

09-MAR-1999; 99US-0123548P.

PR

23-MAR-1999; 99US-0125788P.

PR

25-MAR-1999; 99US-0126264P.

PR

29-MAR-1999; 99US-0126785P.

PR

01-APR-1999; 99US-0127462P.

PR

06-APR-1999; 99US-0128234P.

PR

08-APR-1999; 99US-0128714P.

PR

16-APR-1999; 99US-0129845P.

PR

19-APR-1999; 99US-0130077P.

PR

21-APR-1999; 99US-0130449P.

PR

23-APR-1999; 99US-0130510P.

PR

28-APR-1999; 99US-0130891P.

PR

30-APR-1999; 99US-0131449P.

PR

04-MAY-1999; 99US-0132048P.

PR

05-MAY-1999; 99US-0132407P.

PR

06-MAY-1999; 99US-0132485P.

PR

07-MAY-1999; 99US-0132487P.

PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140931P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.

PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
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PR 27-AUG-1999; 99US-0151080P.
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PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
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PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155113P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 28-OCT-1999; 99US-0162142P.

Query Match 71.6%; Score 58; DB 3; Length 332;
Best Local Similarity 66.7%; Pred. No. 0.056;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
: || |||: |||
Db 26 EKRDLYDQFGHEAFE 40

RESULT 57
AAG14803
ID AAG14803 standard; protein; 367 AA.
XX AC AAG14803;
XX DT 17-OCT-2000 (first entry)
XX XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 14803.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX XX
XX EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
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PR 25-MAY-1999; 99US-0136021P.
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PR 28-MAY-1999; 99US-0137222P.
PR 01-JUN-1999; 99US-0137282P.
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PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
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PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
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PR 02-AUG-1999; 99US-0146386P.
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PR 13-AUG-1999; 99US-0148565P.
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PR 16-AUG-1999; 99US-0149368P.
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PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
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PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
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PR 22-SEP-1999; 99US-0155139P.
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PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158389P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
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PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
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PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
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PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 71.6%; Score 58; DB 3; Length 367;
Best Local Similarity 66.7%; Pred. No. 0.062;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
: ||| : ||| |||

Db 61 EKRDLYDQFGHEAPE 75

RESULT 58
ABBS5579

ID ABB5579 standard; protein; 379 AA.

XX AC ABB5579;

XX 29-AUG-2003 (revised)

DT 16-MAY-2002 (first entry)

XX Lactococcus lactis protein dnaJ.

DE XX

XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.

KW XX

XX Lactococcus lactis; IL1403.

OS XX

PN FR2807446-A1.

XX 12-OCT-2001.

PD XX

XX 11-APR-2000; 2000FR-00004630.

PF XX

XX 11-APR-2000; 2000FR-00004630.

PR XX

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

PA Bolotine A, Sorokine A, Renault P, Ehrlich SD;

XX WPI; 2002-043418/06.

DR XX

XX New nucleotide sequence useful in the identification or Lactococcus

PT lactis and related species.

XX

XX Claim 6; SEQ ID NO 2281; 2504pp; French.

PS

CC The present invention is related to a Lactococcus lactis nucleotide

CC sequence (ABA90521) and related proteins (ABBS53300-ABBS5621). The nucleic

CC acid sequence is useful in the detection and/or amplification of nucleic

CC acid sequence, particularly to identify Lactococcus lactis or related

CC species. The proteins of the invention are useful for the biosynthesis or

CC biodegradation of a composition of interest. The invention helps research

CC in lactic bacteria, particularly useful in the production of yogurt and

CC cheese. Note: The sequence data for this patent is based on equivalent

CC patent WO2001/7334 (published 18-OCT-2001) which is available in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to

CC standardise OS field)

XX

XX Sequence 379 AA;

Query Match 71.6%; Score 58; DB 5; Length 379;

Best Local Similarity 91.7%; Pred. No. 0.065;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGEA 12

Db 60 OKRAAYDQYGEA 71

RESULT 59
ADS29490

ID ADS29490 standard; protein; 379 AA.

XX AC ADS29490;

XX 02-DEC-2004 (first entry)

DT XX

XX Bacterial polypeptide #18523.

DE XX

XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

pathogen tolerance; pest tolerance; plant disease resistance;

cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

XX bacterial polypeptide.

XX Bacteria.

OS XX

XX US2003233675-A1.

PN XX

XX 18-DEC-2003.

PD XX

XX 20-FEB-2003; 2003US-00369493.

PF XX

XX 21-FEB-2002; 2002US-0360039P.

PR XX

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI WPI; 2004-061375/06.

DR XX

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX

XX Claim 1; SEQ ID NO 18523; 122pp; English.

PS

CC The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a

CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the

CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of

CC homologous recombination, modified seed oil or protein yield and/or

CC content, improved yield by modification of carbohydrate, nitrogen or

CC phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress

CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the

CC scope of the invention. Note: The sequence data for this patent did not

CC form part of the printed specification but was obtained in electronic

CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX

XX Sequence 379 AA;

Query Match 71.6%; Score 58; DB 8; Length 379;

Best Local Similarity 91.7%; Pred. No. 0.065;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGEA 12

Db 60 OKRAAYDQYGEA 71

RESULT 60
ADS27721

ID ADS27721 standard; protein; 385 AA.

XX AC ADS27721;

XX 02-DEC-2004 (first entry)
XX Bacterial polypeptide #16754.
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
XX US2003233675-A1.
XX 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
XX 21-FEB-2002; 2002US-0360039P.
XX (CAO Y.) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 16754; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: the sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 385 AA;

Query Match 71.6%; Score 58; DB 8; Length 385;
Best Local Similarity 83.3%; Pred. No. 0.066;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 OKRAAYDOYGH 12
DB 59 QKRAAYDRFGHA 70

RESULT 61
AAG14802
ID AAG14802 standard; protein; 456 AA.
XX
AC AAG14802;
XX
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14802.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EPI033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127482P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
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PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
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PR 18-MAY-1999; 99US-0134768P.
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PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
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PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
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PR 18-JUN-1999; 99US-0139763P.
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PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140333P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140911P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142803P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144894P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145918P.
PR 28-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147303P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.

PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 71.6%; Score 58; DB 3; Length 456;
Best Local Similarity 66.7%; Pred. No. 0.079;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db :|||:|||||
150 EKRDYDQFGHAAFE 164

RESULT 62
ADS30613
ID ADS30613 standard; protein; 369 AA.
XX
AC ADS30613;

XX 02-DEC-2004 (first entry)
XX Bacterial polypeptide #19646.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAO Y.) CAO Y.
XX (HINKLE G J.) HINKLE G J.
XX (SLATER S C.) SLATER S C.
XX (CHEN X.) CHEN X.
XX (GOLDMAN B S.) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 19646; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 369 AA;
XX
XX Query Match 70.4%; Score 57; DB 8; Length 369;
XX Best Local Similarity 90.9%; Pred. No. 0.095;
XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGH 12
Db 62 KRAAYDQFGHA 72
|||||:|||||

RESULT 63

ABB48799

XX ABB48799 standard; protein; 377 AA.
AC ABB48799;
XX

DT 05-FEB-2002 (first entry)

XX Listeria monocytogenes protein #1503.

XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.

XX Listeria monocytogenes.

OS WO200177335-A2.

XX 18-OCT-2001.

XX 11-APR-2001; 2001WO-FR001118.

XX 11-APR-2000; 2000FR-00004629.

XX (INSP) INST PASTEUR.

XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dusart O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX WPI; 2002-010914/01.

XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment

XX and prevention of Listeria and related bacterial infections, and related
XX polypeptides.

XX Claim 6; SEQ ID NO 1504; 192pp; French.

XX The present invention relates to the genome sequence of Listeria
XX monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
XX it are useful for selecting probes and primers for detecting genes in L.
XX monocytogenes and related organisms, and for studying genetic
XX polymorphisms and other genomes. The present sequence is a protein
XX encoded by the genome sequence of the present invention. Proteins
XX expressed from the genome sequence are useful for raising specific
XX antibodies, identification of L. monocytogenes and related organisms, and
XX for biosynthesis and biodegradation, especially biosynthesis of Vitamin
XX B12. The genome sequence and proteins encoded by it are also useful for
XX selecting compounds that regulate gene expression and cell replication
XX and modulate L. monocytogenes-related diseases. In addition, the genome
XX sequence and proteins encoded by it are useful in pharmaceutical and
XX vaccine compositions for the treatment or prevention of infections by L.
XX monocytogenes and related organisms. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 377 AA;

XX Query Match 70.4%; Score 57; DB 5; Length 377;

XX Best Local Similarity 90.9%; Pred. No. 0.098;

XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11

Db 60 QKRAAYDQYGH 70
|||||:|||||

RESULT 64
AAW22358
ID AAW22358 standard; protein; 352 AA.
XX
AC AAW22358;
XX
DT 01-OCT-1997 (first entry)
XX
DE S. pneumoniae N-terminal portion of DnaJ protein.
XX
KW Streptococcus pneumoniae; S. pyogenes; S. agalactiae; genome; HSP72;
KW open reading frame; heat shock protein 72; DnaJ; DnaK; chimaeric;
KW E. coli; Lactococcus lactis; antibody; vaccine; infection; human.
XX
OS Streptococcus pneumoniae.
XX
FN W09640928-A1.
XX
PD 19-DEC-1996.
XX
PF 17-MAY-1996; 96WO-CA000322.
XX
PR 07-JUN-1995; 95US-00472534.
PR 04-AUG-1995; 95US-0001805P.
XX
PA (IAFB-) IAF BIOVAC INC.
XX
PI Hamel J, Brodeur B, Martin D, Rioux C;
XX
DR WPI; 1997-052328/05.
DR N-PSDB; AAT73388.
XX
PT Streptococcal heat shock proteins and corresponding DNA sequences - used
PT in the production of a vaccine to treating and preventing strain-specific
PT Streptococcal infection.
XX
PS Example 3; Page 93-94; 156pp; English.
XX
CC This amino acid sequence corresponds to the N-terminal portion of the
CC Streptococcus pneumoniae DnaJ protein. The protein shows a high degree of
CC identity (72% and 51%) to the DnaJ proteins from Lactococcus lactis and
CC E. coli respectively. The sequence encoding this truncated protein was
CC isolated on the same nucleotide sequence that encodes the S. pneumoniae
CC heat shock protein 72 (HSP72; AAW22357). The nucleotide fragment was
CC isolated from a HindIII-partially digested genomic DNA library using a
CC fragment of the chimaeric gene (AA773392) corresponding to the sequence
CC encoding the C-terminal 169 amino acids of HSP72. The HSP72 protein and
CC its fragment, or antibodies specific to HSP72, are used in pharmaceutical
CC compositions, pref. a vaccine, for treating or preventing infection by S.
CC pneumoniae or related bacteria in humans, e.g. S. pyogenes or S.
CC agalactiae
XX
SQ Sequence 352 AA;
XX
Query Match 69.1%; Score 56; DB 2; Length 352;
Best Local Similarity 91.7%; Pred. No. 0.14;
Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGH 12
DB 60 QKRAAYDQYGAA 71
RESULT 65
ADN26652
ID ADN26652 standard; protein; 362 AA.
XX
AC ADN26652;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #9305.

XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
FN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 9305; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 362 AA;
XX

Query Match 69.1%; Score 56; DB 8; Length 362;
Best Local Similarity 66.7%; Pred. No. 0.14;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 61 KKKLYDTHGHAAFE 75

RESULT 66
ABU00882

ID ABU00882 standard; protein; 378 AA.
 XX AC ABU00882;
 XX DT 23-OCT-2003 (revised)
 XX DT 11-FEB-2003 (first entry)
 XX S. pneumoniae type 4 strain protein from coding region #450.
 XX DE Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
 XX KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
 XX KW gene therapy; vaccine.
 XX OS Streptococcus pneumoniae; type 4 strain.
 XX PN WO200277021-A2.
 XX PD 03-OCT-2002.
 XX PF 27-MAR-2002; 2002WO-IB002163.
 XX PR 27-MAR-2001; 2001GB-00007658.
 XX PA (CHIR-) CHIRON SPA.
 XX PA (GENO-) INST GENOMIC RES.
 XX PI Masignani V, Tettelin H, Fraser C;
 XX WPI: 2003-040579/03.
 XX DR N-PSDB; ABX06162.
 XX New proteins and nucleic acid molecules from Streptococcus pneumoniae,
 PT useful as medicaments for treating or preventing a disease or infection
 PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
 PT ear infection.
 XX Claim 1; SEQ ID NO 900; 56pp; English.
 XX The invention relates to a protein comprising or having at least 50%
 CC identity to any of the 2469 amino acid sequences, identified in the
 CC specification (available on a computer readable format), or its fragment,
 CC expressed from 2469 of 2489 identified DNA coding regions from the
 CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
 CC ABS56454. Also included are an antibody which binds one of the proteins,
 CC treating a patient by administering the protein, DNA or antibody (in a
 CC composition), a kit comprising first and second primers, which are the
 CC nucleic acid cited above or fragments between nucleotides 8-100 of a
 CC sequence not defined in the specification, for amplifying a target
 CC sequence contained within a Streptococcus nucleic acid sequence, where
 CC the first primer is substantially complementary to the target sequence
 CC and the second primer is substantially complementary to the complement of
 CC the target sequence, and where the parts of the primers having
 CC substantial complementarity define the termini of the target sequence to
 CC be amplified, assay comprising contacting a test compound with the
 CC protein, and determining whether the test compound binds to the protein
 CC and a Streptococcus pneumoniae bacterium, where one or more genes
 CC encoding the proteins has been rendered inactive. The proteins, nucleic
 CC acid molecules, antibody and compositions are useful as medicaments for
 CC treating or preventing a disease or infection due to streptococcus
 CC bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis
 CC media or ear infection. They are also useful in developing vaccines,
 CC diagnostics and antibiotics. The methods are useful for identifying
 CC immunodominant proteins. The present sequence is one of the 2469 proteins
 CC expressed by the identified coding regions from the genomic sequence.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
 CC standardise OS field)
 XX SQ Sequence 378 AA;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHA 12
 |||||
 Db 60 QKRAAYDQYGAA 71
 RESULT 67
 ABP81556
 ID ABP81556 standard; protein; 378 AA.
 XX AC ABP81556;
 XX DT 04-MAR-2003 (first entry)
 XX DE Streptococcus pneumoniae polypeptide SEQ ID NO 634.
 XX KW Streptococcus pneumoniae; infection; otitis media; antibacterial;
 XX KW diagnosis; gene therapy.
 XX OS Streptococcus pneumoniae.
 XX PN WO200283855-A2.
 XX PD 24-OCT-2002.
 XX PF 12-APR-2002; 2002WO-US011524.
 XX PR 16-APR-2001; 2001US-0283948P.
 XX PR 18-APR-2001; 2001US-0284443P.
 XX PA (AMCY) AMERICAN CYANAMID CO.
 XX PI Zagursky RJ, Masi AW, Green BA, Chakravarti DN, Russell DP;
 XX Wooters JL;
 XX WPI: 2003-093010/08.
 XX DR N-PSDB; ABZ42404.
 XX New Streptococcus pneumoniae polynucleotides, useful for treating or
 PT preventing S. pneumoniae infections, or non-systemic diseases, e.g.
 PT otitis media, which are induced or exacerbated by S. pneumoniae.
 XX Claim 42; Page 886-888; 1091pp; English.
 XX The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of
 CC a Streptococcus pneumoniae genomic sequence, a fragment or degenerate
 CC variant of the polynucleotide or a nucleic acid sequence 95% identical to
 CC one of the polynucleotides. The S. pneumoniae polynucleotides and encoded
 CC polypeptides (ABP81299-ABP81674) are useful for treating or preventing S.
 CC pneumoniae infections or non-systemic diseases, e.g. otitis media, which
 CC are induced or exacerbated by S. pneumoniae. These are also useful for
 CC detecting S. pneumoniae in a biological sample or diagnosing S.
 CC pneumoniae infection in a subject. The polynucleotides have antibacterial
 CC activity and are useful in gene therapy
 XX SQ Sequence 378 AA;
 Query Match 69.1%; Score 56; DB 6; Length 378;
 Best Local Similarity 91.7%; Pred. No. 0.15;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHA 12
 |||||
 Db 60 QKRAAYDQYGAA 71
 RESULT 68
 ADK48132
 ID ADK48132 standard; protein; 378 AA.
 XX AC ADK48132;
 XX

Pf	29-OCT-2001; 2001WO-GB004789.
Px	
Pr	27-OCT-2000; 2000GB-00026333.
Pr	24-NOV-2000; 2000GB-00028727.
Pr	07-MAR-2001; 2001GB-00005640.
Px	
Pa	(CHIR-) CHIRON SPA.
Pa	(GENO-) INST GENOMIC RES.
Px	
Pi	Telford J, Massignani V, Margarit Y Rosl, Grandi G, Fraser C;
Pi	Tettelin H;
Px	
Dr	WPI; 2002-352536/38.
Dr	N-ESDB; ABN69483.
Px	
Pt	New Streptococcus protein for the treatment or prevention of infection or
Pt	disease caused by Streptococcus bacteria, such as meningitis, and for
Pt	detecting a compound that binds to the protein.
Px	
Cc	Claim 1; Page 3850; 4525pp; English.
Cc	
Cc	The invention relates to a protein (ABP25413-ABP30895) from group B
Cc	streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
Cc	(Streptococcus pyogenes), comprising one of 5483 sequences {S1}, given in
Cc	the specification. The proteins have antibacterial and antiinflammatory
Cc	activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
Cc	antibodies that bind (I) are used in the manufacture of medicaments for
Cc	the treatment or prevention of infection or disease caused by
Cc	Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
Cc	Nucleic acids encoding (I) are used to detect Streptococcus in a
Cc	biological sample. (I) is used to determine whether a compound binds to
Cc	(I). A composition comprising (I) or a nucleic acid encoding (I), may be
Cc	used as a vaccine or diagnostic composition. The disease caused by
Cc	Streptococcus that is prevented or treated may be meningitis. Nucleic
Cc	acid encoding (I) may be used to recombinantly produce (I) and may be
Cc	used in gene therapy. Antibodies to (I) are used for affinity
Cc	chromatography, immunoassays, and distinguishing/identifying
Cc	Streptococcus proteins
Px	
Sq	Sequence 379 AA;
	Query Match 69.1%; Score 56; DB 5; Length 379;
	Best Local Similarity 91.7%; Pred. No. 0.15;
	Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Qy	1 OKRAAYDQYGH 12
Dd	60 OKRAAYDQYGAA 71
	RESULT 70
ADR94852	
ID	ADR94852 standard; protein; 379 AA.
Px	
Px	ADR94852;
Px	
DT	16-DEC-2004 (first entry)
Px	
DE	Novel S. pneumoniae protein sequence, SEQ ID 3487.
Px	
Kw	Meningitis; bacteraemia; pneumonia; otitis media; vaccine;
Kw	bacterial infection.
Px	
OS	Streptococcus pneumoniae.
Px	
XX	US6800744-B1.
PN	
PD	05-OCT-2004.
Px	
Px	30-JUN-1998; 98US-00107433.
Px	
XX	02-JUL-1997; 97US-0051553P.
PR	12-MAY-1998; 98US-0085131P.

07-MAR-2001; 2001GB-00005640.
(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C; Tettelin H;
WPI; 2002-352536/39.
N-PSDB; ABN69484.
New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
Claim 1; Page 3851; 4525pp; English.
The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins
Sequence 396 AA;
Query Match 69.1%; Score 56; DB 5; Length 396;
Best Local Similarity 91.7%; Pred. NO. 0.16;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Qy 1 QKRAAYDQYCHA 12
Db 78 QKRAAYDQYGAA 89
RESULT 72
ADL05213
ID ADL05213 standard; protein; 407 AA.
XX ADL05213;
XX
XX 06-MAY-2004 (first entry)
XX M. catarrhalis protein #979.
XX Moraxella catarrhalis; infection.
XX Moraxella catarrhalis.
XX US6673910-B1.
XX 06-JAN-2004.
XX 04-APR-2000; 2000US-00540236.
XX 08-APR-1999; 99US-0128416P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX Breton GL;
WPI; 2004-178127/17.
XX

(GENO-) GENOME THERAPEUTICS CORP.
Doucette-Stamm LA, Bush D;
WPI; 2004-697205/68.
N-PSDB; ADR92249.
New isolated nucleic acid encoding a Streptococcus pneumoniae polypeptide, useful for diagnosing, preventing and/or treating pathological conditions resulting from the bacterial infection.
Disclosure; SEQ ID NO 3487; 151pp; English.
The invention relates to an isolated nucleic acid comprising a sequence encoding a Streptococcus pneumoniae ADR91366polypeptide, or its fragments, with any of 9 fully defined sequences (appearing as ADR94308, ADR94489, ADR94800, ADR94837, ADR94969, ADR95253, ADR95642, ADR95682, ADR96079) or any of the fully defined sequences appearing as ADR91705, ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or ADR93476 or at least 20 or 30 consecutive nucleotides of the nucleotide sequences, or at least 40, 60 or 300 consecutive nucleotides, which is hybridisable under high stringency conditions to the nucleotide sequence. The nucleic acids and proteins are chosen from 5206 disclosed sequences. Also included are a recombinant expression vector comprising the isolated nucleic acid cited above operably linked to a transcription regulatory element, a cell comprising the recombinant expression vector and a probe comprising at least 20 consecutive nucleotides of the nucleotide sequences as cited above. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of pathological conditions resulting from bacterial infection by Streptococcus pneumoniae e.g. pneumonia, bacteraemia, meningitis and otitis media. The present sequence is one of the 2603 disclosed S. pneumoniae protein sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6800744B1.
Sequence 379 AA;
Query Match 69.1%; Score 56; DB 8; Length 379;
Best Local Similarity 91.7%; Pred. NO. 0.15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QKRAAYDQYCHA 12
Db 61 QKRAAYDQYGAA 72
RESULT 71
ADP28853
ID ABP28853 standard; protein; 396 AA.
XX ABP28853;
XX
XX 02-JUL-2002 (first entry)
XX Streptococcus polypeptide SEQ ID NO 6882.
XX Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX Streptococcus pyogenes.
XX WO200234771-A2.
XX 02-MAY-2002.
XX 29-OCT-2001; 2001WO-GB004789.
XX 27-OCT-2000; 2000GB-00026333.
XX 24-NOV-2000; 2000GB-00028727.
XX

RESULT 75

ABR55123
ID ABR55123 standard; peptide; 15 AA.

XX AC ABR55123;

XX DT 03-JUL-2003 (first entry)

XX DE E. coli dnaJp2 antigen-specific epitope peptide.

XX KW Antigen-specific epitope; immune response; T cell; cytokine;
KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
KW cytostatic; antithyroid; anti-asthmatic; immunosuppressive;
KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
KW antiallergic; dermatological; antipsoriatic.

XX OS Escherichia coli.

XX PN WO2003026579-A2.

XX PD 03-APR-2003.

XX PF 25-SEP-2002; 2002WO-US030578.

XX PR 25-SEP-2001; 2001US-0325499P.

XX PR 11-DEC-2001; 2001US-0339284P.

XX (REGC) UNIV CALIFORNIA.

XX PA Albani S, Martins A;

XX PI WPI; 2003-430097/40.

XX DR Modulating an immune response in a subject having an immune-related
PT disorder, e.g. arthritis by administering an antigen-specific epitope and
PT a cytokine or an agent that effects cytokine activity or expression.

XX PS Disclosure; Page 9; 41pp; English.

XX CC The invention relates to a novel method for modulating an immune response
CC in a subject having an immune-related disorder. The method comprises: (a)
CC administering an antigen-specific epitope, where administration provides
CC epitope-specific T cell immune modulation; and (b) administering a
CC cytokine, an agent that effects cytokine activity or expression, or an
CC anticytokine therapy. The method of the invention has antiarthritic,
CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,
CC dermatological, and antipsoriatic activity. The method is useful for
CC modulating an immune response in a subject having an immune-related
CC disorder. The present sequence is used in the exemplification of the
CC invention

XX SQ Sequence 15 AA;

Query Match 66.7%; Score 54; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.01;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10

DB 6 QKRAAYDQYG 15

RESULT 76

AAG48466
ID AAG48466 standard; protein; 332 AA.

XX AC AAG48466;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 61205.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
XX PR 23-MAR-1999; 99US-0125788P.
XX PR 25-MAR-1999; 99US-0126284P.
XX PR 29-MAR-1999; 99US-0126785P.
XX PR 01-APR-1999; 99US-0127462P.
XX PR 06-APR-1999; 99US-0128234P.
XX PR 08-APR-1999; 99US-0128714P.
XX PR 16-APR-1999; 99US-0129845P.
XX PR 19-APR-1999; 99US-0130077P.
XX PR 21-APR-1999; 99US-0130449P.
XX PR 23-APR-1999; 99US-0130510P.
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PR 21-JUN-1999; 99US-0139817P.
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PR 28-OCT-1999; 99US-0161992P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 54; DB 3; Length 332;
Best Local Similarity 66.7%; Pred. No. 0.3;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
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Db 26 EKRDLYDQVGHEAFE 40

RESULT 77

AAG48465
ID AAG48465 standard; protein; 367 AA.
XX AC AAG48465;
XX AC
DT 18-OCT-2000 (first entry)
XX :
DE Arabidopsis thaliana protein fragment SEQ ID NO: 61204.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX

OS	Arabidopsis thaliana.		
XX	EP1033405-A2.		
XX	06-SEP-2000.		
XX	25-FEB-2000; 2000EP-00301439.		
PR	25-FEB-1999;	99US-0121825P.	99US-0141287P.
PR	05-MAR-1999;	99US-0123180P.	99US-0141842P.
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PR 15-SEP-1999; 99US-0154018P.
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Query Match 66.7%; Score 54; DB 3; Length 367;
 Best Local Similarity 66.7%; Pred. No. 0.33;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15
 :||| ||| ||| |||
 Db 61 EKRDLYDQVGHEAPE 75

RESULT 78
 AAY34469
 ID AAY34469 standard; protein; 383 AA.

XX AC AAY34469;
 XX DT 27-AUG-2003 (revised)
 DT 20-MAR-2003 (revised)
 DT 25-AUG-1999 (first entry)
 XX XX
 DE Porphyromonas gingivalis protein PG124.
 XX Porphyromonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
 KW antigenic.
 XX Porphyromonas gingivalis.
 OS
 XX WO9929870-A1.
 PN
 XX 17-JUN-1999.
 PD
 XX

PF 10-DEC-1998; 98WO-AU001023.
 XX
 PR 10-DEC-1997; 97AU-00000839.
 PR 31-DEC-1997; 97AU-00001182.
 PR 30-JAN-1998; 98AU-00001546.
 PR 10-MAR-1998; 98AU-00002264.
 PR 09-APR-1998; 98AU-00002911.
 PR 23-APR-1998; 98AU-00003128.
 PR 05-MAY-1998; 98AU-00003338.
 PR 22-MAY-1998; 98AU-00003654.
 PR 29-JUL-1998; 98AU-00004917.
 PR 30-JUL-1998; 98AU-00004963.
 PR 04-AUG-1998; 98AU-00005028.
 XX
 PA (CSLC-) CSL LTD.
 XX
 PI Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;
 PI Hocking DM, Webb EA;
 XX
 DR WPI; 1999-385613/32.
 DR N-PSDB; AAX91687.
 XX
 PT Antigenic Porphyromonas gingivalis peptides for preventing gingivitis.
 XX
 PS Claim 1; Page 447-448; 588pp; English.
 XX
 CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic
 CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAY34318 to
 CC AAY34583. AAX91802 to AAX91989 represent PCR primers used in the
 CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
 CC activity with a vaccine mechanism of action. The PG polypeptides can be
 CC used as vaccines especially against Porphyromonas gingivalis. Probes can
 CC be used to detect Porphyromonas gingivalis in standard hybridisation
 CC assays. Porphyromonas gingivalis is involved in periodontal disease
 CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
 CC (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 383 AA;
 Query Match 66.7%; Score 54; DB 2; Length 383;
 Best Local Similarity 75.0%; Pred. No. 0.35;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHGA 12
 |||: |||: |||
 Db 62 QKRSQYDQGHGA 73
 RESULT 79
 AAY34345
 ID AAY34345 standard; protein; 384 AA.
 XX
 AC AAY34345;
 XX
 DT 27-AUG-2003 (revised)
 DT 20-MAR-2003 (revised)
 DT 25-AUG-1999 (first entry)
 XX
 DE Porphyromonas gingivalis protein PG124.
 XX Porphyromonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
 KW antigenic.
 XX Porphyromonas gingivalis.
 OS
 XX WO9929870-A1.
 PN
 XX 17-JUN-1999.
 PD
 XX
 PF 10-DEC-1998; 98WO-AU001023.
 XX
 PR 10-DEC-1997; 97AU-00000839.
 PR 31-DEC-1997; 97AU-00001182.

```
PR 30-JAN-1998; 98AU-00001546.
PR 10-MAR-1998; 98AU-00002264.
PR 09-APR-1998; 98AU-00002911.
PR 23-APR-1998; 98AU-00003128.
PR 05-MAY-1998; 98AU-00003338.
PR 22-MAY-1998; 98AU-00003654.
PR 29-JUL-1998; 98AU-00004917.
PR 30-JUL-1998; 98AU-00004963.
PR 04-AUG-1998; 98AU-00005028.
XX (CSLC-) CSL LTD.
XX
XX Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;
PI Hocking DM, Webb EA;
XX
XX WPI; 1999-385613/32.
DR N-PSDB; AAX91563.
XX
XX Antigenic Porphyromonas gingivalis peptides for preventing gingivitis.
PT
XX Claim 1; Page 305; 588pp; English.
XX
XX AAX91536 to AAX91801 encode two hundred and sixty six antigenic
CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAX34318 to
CC AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
CC activity with a vaccine mechanism of action. The PG polypeptides can be
CC used as vaccines especially against Porphyromonas gingivalis. Probes can
CC be used to detect Porphyromonas gingivalis in standard hybridisation
CC assays. Porphyromonas gingivalis is involved in periodontal disease
CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 384 AA;
SQ
Query Match 66.7%; Score 54; DB 2; Length 384;
Best Local Similarity 75.0%; Pred. No. 0.35;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGH 12
Db 63 QKRSQYDQFGHA 74
RESULT 80
ID AAG48464
ID AAG48464 standard; protein; 456 AA.
XX
XX AAG48464;
AC
XX
XX 18-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 61203.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-00301439.
PF
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR
99US-0128234P.
99US-0128714P.
99US-0129845P.
99US-0130077P.
99US-0130449P.
99US-0130510P.
99US-0130891P.
99US-0131449P.
99US-0132407P.
99US-0132484P.
99US-0132485P.
99US-0132486P.
99US-0132487P.
99US-0132863P.
99US-0134256P.
99US-0134218P.
99US-0134219P.
99US-0134221P.
99US-0134370P.
99US-0134768P.
99US-0134941P.
99US-0135124P.
99US-0135353P.
99US-0135629P.
99US-0136021P.
99US-0136392P.
99US-0136782P.
99US-0137222P.
99US-0137528P.
99US-0137502P.
99US-0137724P.
99US-0138094P.
99US-0138540P.
99US-0138847P.
99US-0139119P.
99US-0139452P.
99US-0139453P.
99US-0139452P.
99US-0139454P.
99US-0139455P.
99US-0139456P.
99US-0139457P.
99US-0139458P.
99US-0139459P.
99US-0139460P.
99US-0139461P.
99US-0139462P.
99US-0139463P.
99US-0139750P.
99US-0139763P.
99US-0139817P.
99US-0139899P.
99US-0140353P.
99US-0140354P.
99US-0140695P.
99US-0140823P.
99US-0140991P.
99US-0141287P.
99US-0141842P.
99US-0142154P.
99US-0142055P.
99US-0142390P.
99US-0142803P.
99US-0142920P.
99US-0142977P.
99US-0143542P.
99US-0143624P.
99US-0144005P.
99US-0144085P.
99US-0144086P.
99US-0144325P.
99US-0144331P.
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PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145911P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149358P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.

PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 22-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 54; DB 3; Length 456;
Best Local Similarity 66.7%; Pred. NO. 0.42;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 OKRAAYDOXGHAPE 15
Db 150 EKRDLYDQVGHAPE 164

RESULT 81

ADS21338
ID ADS21338 standard; protein; 360 AA.

XX ADS21338;

XX 02-DEC-2004 (first entry)

DE Bacterial polypeptide #10371.

XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI 99US-0158369P;
XX

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DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 10371; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
SQ Sequence 360 AA;

Query Match 64.2%; Score 52; DB 8; Length 360;
Best Local Similarity 69.2%; Pred. No. 0.75;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAA 13
DB 59 EKKRYDQYGHQA 71

RESULT 82
ID ADS44776 standard; protein; 372 AA.
AC ADS44776;
XX
XX 02-DEC-2004 (first entry)
DT
DE Bacterial polypeptide #23206.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.
XX
XX Bacteria.
XX
XX US2003233675-A1.
PN
XX
XX 18-DEC-2003.
PD
XX
XX 20-FEB-2003; 2003US-00369493.
PF
XX
XX 21-FEB-2002; 2002US-0360039P.
PR
XX
XX (CAOY/) CAO Y.
PA

(PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 23206; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
SQ Sequence 372 AA;

Query Match 64.2%; Score 52; DB 8; Length 372;
Best Local Similarity 81.8%; Pred. No. 0.77;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11
DB 60 QKRAHYDQFGH 70

RESULT 83
ID ADA33697 standard; protein; 375 AA.
XX
XX ADA33697;
XX
XX 20-NOV-2003 (first entry)
DT
DE Acinetobacter baumannii protein #858.
XX
XX Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
XX plant biocontrol agent.
XX
XX Acinetobacter baumannii.
XX
XX US562958-B1.
PN
XX
XX 13-MAY-2003.
PD
XX
XX 04-JUN-1999; 99US-00328352.
PF
XX
XX 09-JUN-1998; 98US-0088701P.
PR
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XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Breton G, Bush D;
XX XX WPI; 2003-576092/54.
XX DR N-PSDB; ADA29571.
XX PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
XX PT for diagnosing a bacterial disease, as components of antibacterial
XX PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
XX PT plants.
XX PS Example; SEQ ID NO 4984; 328pp; English.
XX CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
XX CC The A. baumannii nucleic acids and polypeptides are useful as reagents
XX CC for diagnosing a bacterial disease, as components of antibacterial
XX CC vaccines, as targets for antibacterial drugs, to detect the presence of
XX CC A. baumannii and other Acinetobacter species in a sample, in screening
XX CC compounds for the ability to interfere with the A. baumannii life cycle
XX CC or to inhibit A. baumannii infection, and as biocontrol agents for
XX CC plants. The present sequence represents the amino acid sequence of an A.
XX CC baumannii protein.
XX SQ Sequence 375 AA;
CC CC Query Match 64.2%; Score 52; DB 6; Length 375;
CC CC Best Local Similarity 60.0%; Pred. No. 0.78;
CC CC Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0
QY QY 1 OKRAAYDQYGHAAFE 15
DB DB :||: ||: ||| |||
DB DB 66 EKRSMDYDRMGHNAFE 80
RESULT 84
ADN18559
ID ADN18559 standard; protein; 376 AA.
AC AC ADN18559;
DT DT 02-DEC-2004 (first entry)
XX Bacterial polypeptide #1212.
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.
XX OS Bacteria.
XX US2003233675-A1.
XX PN 18-DEC-2003.
XX PD 20-FEB-2003; 2003US-00369493.
XX PF 21-FEB-2002; 2002US-0360039P.
XX PR (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.

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XX WPI; 2003-029926/02.
DR N-PSDB; ACA30497.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 54551; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway;
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 297 AA;

Query Match 61.7%; Score 50; DB 6; Length 297;
Best Local Similarity 64.3%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 OKRAAYDQYCHAAF 14
   :||| ||||| :|
Db 58 KKRAQYDQYGSWF 71

RESULT 86
AAG30655
ID AAG30655 standard; protein; 320 AA.
AC AAG30655;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 36688.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX
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25-FEB-2000; 2000EP-00301439.

25-FEB-1999; 99US-0121825P.
05-MAR-1999; 99US-0123180P.
09-MAR-1999; 99US-0123548P.
23-MAR-1999; 99US-0125788P.
25-MAR-1999; 99US-0126264P.
29-MAR-1999; 99US-0126785P.
01-APR-1999; 99US-0127462P.
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QY 1 QKRAAYDQYG 10
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Db 33 QKRAVVDQYG 42

RESULT 87

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XX AC AAG30654;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 36687.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 61 QKRAAYDQYG 70

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ID ABM70982 standard; protein; 379 AA.
XX
AC ABM70982;
XX
DT 20-NOV-2003 (first entry)
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DE Staphylococcus aureus protein #222.
XX
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target.
XX
OS Staphylococcus aureus.
XX
PN W0200294868-A2.
XX
PD 28-NOV-2002.
XX
PF 27-MAR-2002; 2002WO-IB002637.
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PR 27-MAR-2001; 2001GB-00007661.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Masignani V, Mora M, Scarselli M;
XX WPI; 2003-120786/11.
XX N-PSDB; ACF72542.
XX
PT New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX
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PS Claim 1; SEQ ID NO 444; 49pp; English.
XX
CC The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus proteins of the invention
XX
SQ Sequence 379 AA;

Query Match 61.7%; Score 50; DB 6; Length 379;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGH 11
Db 61 KRAAYDQYGH 70

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AC AAG53768;
XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 68486.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match      60.5%; Score 49; DB 3; Length 295;
Best Local Similarity 90.0%; Pred. No. 2.1;
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Qy 1 QKRAAYDQYG 10
Db 33 QKRAIYDQYG 42

RESULT 90
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XX AC AAG18158;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 19453.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX OS Arabidopsis thaliana.
XX PN EPI033405-A2.
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Query Match 60.5%; Score 49; DB 3; Length 295;
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Best Local Similarity 90.0%; Pred. No. 2.5;
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QY 1 QKRAAYDQYG 10
Db 88 QKRAAYDQYG 97
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RESULT 95
ADS28176
ID ADS28176 standard; protein; 370 AA.
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AC ADS28176;
XX
DT 02-DEC-2004 (first entry)
DE
DE Bacterial polypeptide #17209.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.
XX

OS Bacteria.
XX US2003233675-A1.
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 17209; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 370 AA;

Query Match 60.5%; Score 49; DB 8; Length 370;
Best Local Similarity 72.7%; Pred. No. 2.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11
Db 60 QKRAHYDQFGH 70
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RESULT 96
ADS23586
ID ADS23586 standard; protein; 423 AA.
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XX ADS23586;
XX
XX 02-DEC-2004 (first entry)
DE
DE Bacterial polypeptide #12619.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
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Best Local Similarity 80.0%; Pred. NO. 4.6;
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Db 8 QKXAVYDQYG 17

RESULT 98

AAG16068

ID AAG16068 standard; protein; 292 AA.

XX

AC AAG16068;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 16566.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS EPI033405-A2.
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KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
KW	termination sequence.			
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Query Match 58.0%; Score 47; DB 3; Length 309;

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XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 16564.

DE Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

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Search completed: September 2, 2005, 20:55:22
Job time : 170 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 2, 2005, 20:48:42 ; Search time 22 Seconds
(without alignments)
50.897 Million cell updates/sec

Title: US-09-616-247-4

Perfect score: 81

Sequence: 1 QKRAAYDQYGHAAFE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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51	38	46.9	107	3	US-08-982-129-3	Sequence 3, Appli
52	38	46.9	108	3	US-08-893-534A-5	Sequence 5, Appli
53	38	46.9	108	3	US-08-996-679-5	Sequence 5, Appli
54	38	46.9	108	3	US-08-939-853A-7	Sequence 7, Appli
55	38	46.9	108	3	US-09-115-395-5	Sequence 5, Appli
56	38	46.9	108	3	US-09-113-977C-38	Sequence 38, Appl
57	38	46.9	108	3	US-09-507-102-5	Sequence 5, Appli
58	38	46.9	108	3	US-09-250-059-5	Sequence 5, Appli
59	38	46.9	108	3	US-09-248-074-5	Sequence 5, Appli
60	38	46.9	108	4	US-09-357-717-5	Sequence 5, Appli
61	38	46.9	108	4	US-09-458-870-5	Sequence 5, Appli
62	38	46.9	108	4	US-09-351-048A-38	Sequence 38, Appl
63	38	46.9	108	4	US-09-248-015-5	Sequence 5, Appli
64	38	46.9	108	4	US-09-544-782-5	Sequence 5, Appli
65	38	46.9	108	4	US-10-058-821-5	Sequence 5, Appli
66	38	46.9	108	4	US-10-193-653-38	Sequence 38, Appl
67	38	46.9	109	4	US-09-178-178B-8	Sequence 8, Appli
68	38	46.9	109	4	US-09-457-864-8	Sequence 8, Appli
69	38	46.9	109	4	US-09-457-865A-8	Sequence 8, Appli
70	38	46.9	119	4	US-09-513-999C-5896	Sequence 5896, Ap
71	38	46.9	822	2	US-08-474-067-9	Sequence 9, Appli
72	38	46.9	822	2	US-08-474-068A-9	Sequence 9, Appli
73	38	46.9	822	2	US-08-472-481-8	Sequence 8, Appli
74	38	46.9	75	4	US-09-513-999C-6016	Sequence 6016, Ap
75	37	45.7	242	4	US-09-134-000C-5008	Sequence 5008, Ap
76	37	45.7	320	4	US-09-248-796A-17629	Sequence 17629, A
77	37	45.7	320	4	US-09-198-452A-48	Sequence 48, Appl
78	37	45.7	392	4	US-09-438-185A-34	Sequence 34, Appl
79	37	45.7	406	4	US-09-134-000C-5523	Sequence 5523, Ap
80	37	45.7	434	4	US-09-489-039A-10301	Sequence 10301, A
81	37	45.7	556	4	US-09-244-805-27	Sequence 27, Appl
82	37	45.7	581	4	US-09-252-991A-27230	Sequence 27230, A
83	37	45.7	953	4	US-08-346-849-8	Sequence 8, Appli
84	36	44.4	52	1	US-08-293-28A-8	Sequence 8, Appli
85	36	44.4	52	2	US-08-898-300-8	Sequence 8, Appli
86	36	44.4	52	4	US-08-824-513-8	Sequence 8, Appli
87	36	44.4	65	4	US-09-513-999C-5565	Sequence 5565, Ap
88	36	44.4	130	4	US-09-270-767-47445	Sequence 47445, A
89	36	44.4	147	4	US-09-513-999C-6925	Sequence 6925, Ap
90	36	44.4	152	4	US-09-270-767-46278	Sequence 46278, A
91	36	44.4	153	4	US-09-621-976-5129	Sequence 5129, Ap
92	36	44.4	175	4	US-09-270-767-32870	Sequence 32870, A
93	36	44.4	175	4	US-09-270-767-48087	Sequence 48087, A
94	36	44.4	304	4	US-09-543-681A-7507	Sequence 7507, Ap
95	36	44.4	330	4	US-09-248-796A-19977	Sequence 19977, A
96	36	44.4	337	4	US-09-665-478A-8	Sequence 8, Appli
97	36	44.4	387	4	US-09-489-039A-10623	Sequence 10623, A
98	36	44.4	412	4	US-09-252-991A-26237	Sequence 26237, A
99	36	44.4	487	4	US-09-252-991A-21980	Sequence 21980, A
100	36	44.4				

ALIGNMENTS

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RESULT 1
US-08-618-464-4
; Sequence 4, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-08-618-464-4

Query Match 100.0%; Score 81; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 2
US-09-107-615-4
; Sequence 4, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
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; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-09-107-615-4

Query Match 100.0%; Score 81; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 3
US-09-756-983-10
; Sequence 10, Application US/09756983
; Patent No. 6787154
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
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; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJpl heat shock protein
US-09-756-983-10

Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 4
PCT-US95-04896-4
; Sequence 4, Application PC/TUS9504896
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY
; APPLICANT: OF CALIFORNIA
; TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
; TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04896
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BERLINER, ROBERT
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-314
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-977-1001
; TELEFAX: 213-977-1003
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
PCT-US95-04896-4

Query Match 100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 5
US-09-553-498-4
; Sequence 4, Application US/09553498

; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted prot
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 131
; TYPE: PRT
; ORGANISM: E. coli
US-09-553-498-4

Query Match 100.0%; Score 81; DB 3; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | | | |
Db 84 QKRAAYDQYGHAAFE 98

RESULT 6
US-09-618-869-4
; Sequence 4, Application US/09618869
; Patent No. 6455279
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-618-869-4

Query Match 100.0%; Score 81; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | | | |
Db 84 QKRAAYDQYGHAAFE 98

RESULT 7
US-09-543-681A-5912
; Sequence 5912, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05

;
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5912
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5912

Query Match 100.0%; Score 81; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 63 QKRAAYDQYGHAAFE 77

RESULT 8
US-09-489-039A-9011
; Sequence 9011, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9011
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9011

Query Match 100.0%; Score 81; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 64 QKRAAYDQYGHAAFE 78

RESULT 9
US-09-553-498-2
; Sequence 2, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted prote
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 399
; TYPE: PRT
; ORGANISM: E. coli
US-09-553-498-2

Query Match 100.0%; Score 81; DB 3; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 84 QKRAAYDQYGHAAFE 98

RESULT 10
US-09-618-869-2
; Sequence 2, Application US/09618869
; Patent No. 6455279
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
; TITLE OF INVENTION: CHAPERONES
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-618-869-2

Query Match 100.0%; Score 81; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 84 QKRAAYDQYGHAAFE 98

RESULT 11
US-08-618-464-5
; Sequence 5, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-08-618-464-5

Query Match 88.9%; Score 72; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.2e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
:|||||
Db 2 ERAAYDQYGHAAFE 15

RESULT 12
; Sequence 5, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide

; LOCATION: 1..15
US-09-107-615-5

Query Match 88.9%; Score 72; DB 3; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.2e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
:|||||
Db 2 ERAAYDQYGHAAFE 15

RESULT 13
PCT-US95-04896-5
; Sequence 5, Application PC/TUS9504896
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY
; APPLICANT: OF CALIFORNIA
; TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
; TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04896
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BERLINER, ROBERT
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-314
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-977-1001
; TELEFAX: 213-977-1003
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
PCT-US95-04896-5

Query Match 88.9%; Score 72; DB 5; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.2e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
:|||||
Db 2 ERAAYDQYGHAAFE 15

RESULT 14
US-09-252-991A-27174
; Sequence 27174, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27174
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27174

Query Match 76.5%; Score 62; DB 4; Length 381;
Best Local Similarity 78.6%; Pred. No. 0.0041;
Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
|||||
Db 66 KRAAYDQYGHAGVD 79

RESULT 15
US-08-472-534-6
; Sequence 6, Application US/08472534
; Patent No. 5919620
; GENERAL INFORMATION:
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; TITLE OF INVENTION: HEAT SHOCK PROTEIN HSP72 FROM
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,534
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr. James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Biovac-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-534-6

Query Match 69.1%; Score 56; DB 2; Length 352;
Best Local Similarity 91.7%; Pred. No. 0.044;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 QKRAAYDQYGHGA 12
```

```
Db 60 QKRAAYDQYGHGA 71
|||||
US-09-583-110-4647
; Sequence 4647, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4647
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4647

Query Match 69.1%; Score 56; DB 4; Length 378;
Best Local Similarity 91.7%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHGA 12
|||||
Db 60 QKRAAYDQYGHGA 71

RESULT 17
US-09-107-433-3487
; Sequence 3487, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
```

TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3487:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...379
SEQUENCE DESCRIPTION: SEQ ID NO: 3487:
US-09-107-433-3487

Query Match 69.1%; Score 56; DB 4; Length 379;
Best Local Similarity 91.7%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHGA 12
DB 61 QKRAAYDQYGHGA 72

RESULT 18
US-09-540-236-2899
Sequence 2899, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2899
LENGTH: 407
TYPE: PRT
ORGANISM: M.catarrhalis
US-09-540-236-2899

Query Match 69.1%; Score 56; DB 4; Length 407;
Best Local Similarity 60.0%; Pred. No. 0.052;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15
DB 84 EKRAATYDRMGHSAVE 98

RESULT 19
US-09-861-451A-2
Sequence 2, Application US/09861451A
Patent No. 6759516
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific & Industrial Research Orga
TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences
FILE REFERENCE: FP34033/01
CURRENT APPLICATION NUMBER: US/09/861,451A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: PF7273
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 2
LENGTH: 368
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Deduced protein
OTHER INFORMATION: sequence from clone PAD612

US-09-861-451A-2

Query Match 67.9%; Score 55; DB 4; Length 368;
Best Local Similarity 64.3%; Pred. No. 0.07;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAPE 15
DB 67 KRQYDKFGHAAFD 80

RESULT 20
US-08-618-464-6
Sequence 6, Application US/08618464
Patent No. 5773570
GENERAL INFORMATION:
APPLICANT: CARSON, DENNIS A.
TITLE OF INVENTION: ALBANT, SALVATORE
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
TITLE OF INVENTION: INDUCING
TITLE OF INVENTION: INVOLVED IN
TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,464
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: dnaJp2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1...15
US-08-618-464-6

Query Match 66.7%; Score 54; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
DB 6 QKRAAYDQYG 15

RESULT 21
US-09-107-615-6
Sequence 6, Application US/09107615
Patent No. 6153200

GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIS INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: dnaJp2
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-09-107-615-6

Query Match 66.7%; Score 54; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0035; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
Db 6 QKRAAYDQYG 15

RESULT 22
US-09-248-796A-17703
; Sequence 17703, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 17703
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17703

Query Match 65.4%; Score 53; DB 4; Length 240;
Best Local Similarity 60.0%; Pred. No. 0.1; Mismatches 4; Indels 2; Gaps 0;
Matches 9; Conservative 4; Mismatches 4; Indels 2; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 104 EKRAQYDQFGASAFD 118

RESULT 23
US-09-328-352-4984
; Sequence 4984, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4984
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (322)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-328-352-4984

Query Match 64.2%; Score 52; DB 4; Length 375;
Best Local Similarity 60.0%; Pred. No. 0.24; Mismatches 3; Indels 3; Gaps 0;
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 66 EKRSYDGMGHNAFE 80

RESULT 24
US-09-902-540-13689
; Sequence 13689, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13689
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13689

Query Match 58.0%; Score 47; DB 4; Length 138;
Best Local Similarity 58.3%; Pred. No. 0.65; Mismatches 4; Indels 1; Gaps 0;
Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 0;

QY 1 QKRAAYDQYGHGA 12

Db ::||| ||:||||
66 ERRAKYDFGHA 77

RESULT 25

US-09-710-279-890
; Sequence 890, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 890
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-890

Query Match 58.0%; Score 47; DB 4; Length 373;
Best Local Similarity 80.0%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRAAYDOVGH 11
 ||| ||:||||
Db 61 KRAYDQFGH 70

RESULT 26

US-09-134-001C-3688
; Sequence 3688, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3688
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3688

Query Match 58.0%; Score 47; DB 3; Length 385;
Best Local Similarity 80.0%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRAAYDOVGH 11
 ||| ||:||||
Db 73 KRAYDQFGH 82

RESULT 27

US-09-908-992B-11
; Sequence 11, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH

; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-992B-11

Query Match 54.3%; Score 44; DB 4; Length 387;
Best Local Similarity 57.1%; Pred. No. 6.7;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KRAAYDOYGHAAFE 15
 || ||| ||| |||
Db 84 KRQYDAYGSAGFD 97

RESULT 28

US-09-248-796A-17628
; Sequence 17628, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17628
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17628

Query Match 54.3%; Score 44; DB 4; Length 397;
Best Local Similarity 80.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYQG 10
 ||| ||| |||
Db 65 QKREIYDOYQG 74

RESULT 29

US-09-908-992B-10
; Sequence 10, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-992B-10

Query Match      54.3%; Score 44; DB 4; Length 414;
Best Local Similarity 57.1%; Pred. No. 7.1;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      2 KRAAYDQYGHAAFE 15
Db      84 KRQYDAYGSAGFD 97

RESULT 30
US-08-686-417-3
; Sequence 3, Application US/08686417
; Patent No. 5850018
; GENERAL INFORMATION:
; APPLICANT: Baezczynski, Chris
; APPLICANT: Barbour, Eric
; APPLICANT: Horowitz, Jeannine
; APPLICANT: Robichan, Jeffrey L.
; TITLE OF INVENTION: AN EXPRESSION CONTROL SEQUENCE FOR
; TITLE OF INVENTION: GENERAL AND EFFECTIVE EXPRESSION OF GENES IN PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,417
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 27112-20038.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-686-417-3

Query Match      54.3%; Score 44; DB 2; Length 419;
Best Local Similarity 53.3%; Pred. No. 7.2;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 KRAAYDQYGHAAFE 15
Db      65 EKREIYDQGEDALK 79

RESULT 31
US-09-908-992B-29
; Sequence 29, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Mus sp.
; NAME/KEY: MOD RES
; LOCATION: (206)..(224)
; OTHER INFORMATION: Unknown amino acid
US-09-908-992B-29

Query Match      54.3%; Score 44; DB 4; Length 452;
Best Local Similarity 57.1%; Pred. No. 7.8;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      2 KRAAYDQYGHAAFE 15
Db      150 KRQYDAYGSAGFD 163

RESULT 32
US-09-908-992B-9
; Sequence 9, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-992B-9

Query Match      54.3%; Score 44; DB 4; Length 453;
Best Local Similarity 57.1%; Pred. No. 7.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      2 KRAAYDQYGHAAFE 15
Db      150 KRQYDAYGSAGFD 163

RESULT 33
US-09-908-992B-30
; Sequence 30, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
```

```

; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-992B-30

```

Query Match 54.3%; Score 44; DB 4; Length 453;
Best Local Similarity 57.1%; Pred. No. 7.9;
Matches 8; Conservative 1; Mismatches 5; Indels

```

RESULT 34
US-09-908-992B-28
; Sequence 28, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (206)..(224)
; OTHER INFORMATION: Unknown amino acid
US-09-908-992B-28

```

Query Match 54.3%; Score 44; DB 4; Length 479;
Best Local Similarity 57.1%; Pred. NO. 8.3;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

RESULT 35
US-09-908-992B-8
; Sequence 8, Application US/0908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCES: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20

```

; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 480
; TYPE: prt
; ORGANISM: Homo sapiens
; US-09-008-992B-8

```

Query Match 54.3%; Score 44; DB 4; Length 480;
Best Local Similarity 57.1%; Pred. No. 8.4;
Matches 8; Conservative 1; Mismatches 5; Indels

```

RESULT 36
US-09-908-992B-12
; Sequence 12, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054 .01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-992B-12

```

Query Match 54.3%; Score 44; DB 4; Length 480;
Best Local Similarity 57.1%; Pred. No. 8.4;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

RESULT 37
US-09-882-835-4
; Sequence 4, Application US/09882835
; Patent No. 6462187
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 22109, A NOVEL HUMAN THIOREDOXIN FAMILY
; FILE OF INVENTION: MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-063001
; CURRENT APPLICATION NUMBER: US/09/882,835
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,673
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-882-835-4
Query Match          50.6%;      Score 41;      DB 4;      Length 87;

```

Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRAAYDQYG 10
Db 79 RRAAYDQYG 87

RESULT 38

US-09-658-644-4
; Sequence 4, Application US/09658644
; Patent No. 6537554
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Jeffers, Michael
; TITLE OF INVENTION: Nucleotide Sequences and Amino Acid Sequences of
; TITLE OF INVENTION: Secreted Proteins Involved in Angiogenesis
; FILE REFERENCE: 15966-S17 CIP1
; CURRENT APPLICATION NUMBER: US/09/658,644
; CURRENT FILING DATE: 2001-09-09
; PRIOR APPLICATION NUMBER: U.S.S.N. 09/150,684
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-658-644-4

Query Match 50.6%; Score 41; DB 4; Length 223;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAF 14
Db 82 RRKEYDTLGHSAF 94

RESULT 39

US-09-949-016-6832
; Sequence 6832, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6832
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6832

Query Match 50.6%; Score 41; DB 4; Length 223;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAF 14
Db 82 RRKEYDTLGHSAF 94

RESULT 40

US-09-949-016-11497
; Sequence 11497, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11497
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11497

Query Match 50.6%; Score 41; DB 4; Length 267;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAF 14
Db 126 RRKEYDTLGHSAF 138

RESULT 41

US-08-974-546-1
; Sequence 1, Application US/08974546
; Patent No. 5945287
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: TWO HUMAN HEAT SHOCK PROTEIN HOMOLOGS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,546
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0428
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRA1TUT21
; CLONE: 2525691
US-08-974-546-1

Query Match 50.6%; Score 41; DB 2; Length 348;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
Db 59 KRGGLYDYG 68

RESULT 42

US-09-543-681A-7130
; Sequence 7130, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A

; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 7130
; LENGTH: 387

; TYPE: PRT

; ORGANISM: Proteus mirabilis

US-09-543-681A-7130

Query Match 50.6%; Score 41; DB 4; Length 387;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAF 14
Db 356 QKTAAYGHGFAEF 369

RESULT 43

US-09-252-991A-29230
; Sequence 29230, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29230

; LENGTH: 845

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29230

Query Match 50.6%; Score 41; DB 4; Length 845;
Best Local Similarity 61.5%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 RAAAYDQYGHAAF 15

Db 408 RSAADQLGHGALE 420

RESULT 44

US-09-902-540-14837
; Sequence 14837, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 14837
; LENGTH: 231

; TYPE: PRT

; ORGANISM: Myxococcus xanthus

US-09-902-540-14837

Query Match 49.4%; Score 40; DB 4; Length 231;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGH 11
Db 201 ERAAYEHFGH 210

RESULT 45

US-09-328-352-8169
; Sequence 8169, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8169

; LENGTH: 317

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-8169

Query Match 49.4%; Score 40; DB 4; Length 317;
Best Local Similarity 46.7%; Pred. No. 28;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAF 15
Db 217 EKKAALDKLAHEAFK 231

RESULT 46

US-09-252-991A-18102
; Sequence 18102, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; SEQ ID NO 18102
; LENGTH: 845

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18102

```
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18102
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18102

Query Match 49.4%; Score 40; DB 4; Length 677;
Best Local Similarity 58.3%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 AAYDOYGHAAFE 15
Db 656 AAWDAYAHAAID 667

RESULT 47
US-09-252-991A-24992
; Sequence 24992, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24992
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24992

Query Match 49.4%; Score 40; DB 4; Length 915;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 RAAYDOYGHAAF 14
Db 614 RAAGEERGHAAF 625

RESULT 48
US-09-248-796A-21361
; Sequence 21361, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21361
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21361
```

```
Query Match 48.1%; Score 39; DB 4; Length 116;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDOYQ 10
Db 96 QKYSAYDQWG 105

RESULT 49
US-08-619-554-4
; Sequence 4, Application US/08619554
; Patent No. 5821353
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS, Cameron M.
; APPLICANT: CHREBET, Gary L.
; APPLICANT: CLEMAS, Joseph
; APPLICANT: EL-SHERBEINI, Mohammed
; APPLICANT: FOOR, Forrest
; APPLICANT: KAHN, Jennifer,
; APPLICANT: KELLY, Rosemarie, - PARENT, S.A.
; APPLICANT: MARRINAN, Jean, - RAMADAN, N.M.
; APPLICANT: MORIN, Nancy, - REGISTER, E.A.
; APPLICANT: ONISHI, Janet, - SHEL, Gan-Ju
; TITLE OF INVENTION: DNA ENCODING 1,3 BETA-D GLUCAN
; TITLE OF INVENTION: SYNTHASE SUBUNITS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOSEPH A. COPPOLA - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/619,554
; FILING DATE: 01-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: COPPOLA, JOSEPH A
; REGISTRATION NUMBER: 38,413
; REFERENCE/DOCKET NUMBER: 19104PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-6734
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1895 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-619-554-4

Query Match 48.1%; Score 39; DB 2; Length 1895;
Best Local Similarity 42.9%; Pred. No. 2.8e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 QKRAAYDOYGHAAF 14
Db 31 QDSAYDEYGOPIY 44

RESULT 50
```

US-08-326-117B-3
; Sequence 3, Application US/08326117B
; Patent No. 5693491
; GENERAL INFORMATION:
; APPLICANT: BULLA, LEE A.
; APPLICANT: JI, TAE
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; TITLE OF INVENTION: TOXIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,117B
; FILING DATE: 19-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 7112-0037.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-326-117B-3

Query Match 46.9%; Score 38; DB 1; Length 107;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
Db 70 EKIVKELYGHAVSE 84

RESULT 51
US-08-982-129-3
; Sequence 3, Application US/08982129
; Patent No. 6007981
; GENERAL INFORMATION:
; APPLICANT: BULLA, LEE A.
; APPLICANT: JI, TAE
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; TITLE OF INVENTION: TOXIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/982,129
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/326,117
; APPLICATION NUMBER: US 08/326,117
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 7112-0037.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-982-129-3

Query Match 46.9%; Score 38; DB 3; Length 107;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
Db 70 EKIVKELYGHAVSE 84

RESULT 52
US-08-893-534A-5
; Sequence 5, Application US/08893534A
; Patent No. 6031072
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,534A
; FILING DATE: 11-JUL-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 100086.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-893-534A-5

Query Match 46.9%; Score 38; DB 3; Length 108;

Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 53
US-08-996-679-5
; Sequence 5, Application US/08996679
; Patent No. 6169071
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,679
; FILING DATE: 23-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 100086.401C1
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-996-679-5

Query Match 46.9%; Score 38; DB 3; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 54
US-08-939-853A-7
; Sequence 7, Application US/08939853A
; Patent No. 6203788
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington

; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,853A
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 32,391
; REFERENCE/DOCKET NUMBER: 100086.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-939-853A-7

Query Match 46.9%; Score 38; DB 3; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 55
US-09-115-395-5
; Sequence 5, Application US/09115395A
; Patent No. 6207639
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
; FILE REFERENCE: 100086.401C3
; CURRENT APPLICATION NUMBER: US/09/115,395A
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 08/996,679
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/893,534
; EARLIER FILING DATE: 1997-07-11
; EARLIER APPLICATION NUMBER: 60/021,612
; EARLIER FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-115-395-5

Query Match 46.9%; Score 38; DB 3; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 56
US-09-113-977C-38
; Sequence 38, Application US/09113977C
; Patent No. 6277824

; GENERAL INFORMATION:
; APPLICANT: Doherty, Patrick
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE
; FILE REFERENCE: 100086.403
; CURRENT APPLICATION NUMBER: US/09/113.977C
; CURRENT FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-113-977C-38

Query Match 46.9%; Score 38; DB 3; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 69 EKIVKVELYGHAVSE 83

RESULT 57
US-09-507-102-5
; Sequence 5, Application US/09507102
; Patent No. 6326352
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED IP LAW GROUP PLLC
; STREET: 6300 Bank of America Bldg., 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,102
; FILING DATE: 17-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/893,534
; FILING DATE: 11-JUL-1997
; APPLICATION NUMBER: US 60/021,612
; FILING DATE: 12-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Christensen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 100086.401C10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-507-102-5

Query Match 46.9%; Score 38; DB 3; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 69 EKIVKVELYGHAVSE 83

RESULT 58
US-09-250-059-5
; Sequence 5, Application US/09250059
; Patent No. 6333307
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
; FILE REFERENCE: 100086.401C6
; CURRENT APPLICATION NUMBER: US/09/250,059
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-250-059-5

Query Match 46.9%; Score 38; DB 3; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 69 EKIVKVELYGHAVSE 83

RESULT 59
US-09-248-074-5
; Sequence 5, Application US/09248074
; Patent No. 6346512
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C5
; CURRENT APPLICATION NUMBER: US/09/248,074
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-248-074-5

Query Match 46.9%; Score 38; DB 3; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 69 EKIVKVELYGHAVSE 83

RESULT 60
US-09-357-717-5
; Sequence 5, Application US/09357717
; Patent No. 6417325
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz

```

RESULT 62
US-09-351-048A-38
; Sequence 38, Application US/09351048A
; Patent No. 6472368
; GENERAL INFORMATION:
; APPLICANT: Donerty, Patrick
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE
; TITLE OF INVENTION: FUNCTION
; FILE REFERENCE: 100086.403C1
; CURRENT APPLICATION NUMBER: US/09/351,048A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis

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GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riz.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY
; FILE REFERENCE: 100086.401C12
; CURRENT APPLICATION NUMBER: US/10/058,821
; CURRENT FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-058-821-5

Query Match 46.9%; Score 38; DB 4; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 66
US-10-193-653-38
; Sequence 38, Application US/10193653
; Patent No. 6806255
; GENERAL INFORMATION:
; APPLICANT: Doherty, Patrick
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE
; FILE REFERENCE: 100086.403C2
; CURRENT APPLICATION NUMBER: US/10/193,653
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-10-193-653-38

Query Match 46.9%; Score 38; DB 4; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 67
US-09-178-176B-8
; Sequence 8, Application US/09178176B
; Patent No. 6423502
; GENERAL INFORMATION:
; APPLICANT: BULLA, Lee A.
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; FILE REFERENCE: 27112-20037.11
; CURRENT APPLICATION NUMBER: US/09/178,176B
; CURRENT FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 08/982,129
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: US 08/326,117
; PRIOR FILING DATE: 1994-10-19

NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: M. sexta
US-09-178-176B-8

Query Match 46.9%; Score 38; DB 4; Length 109;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 70 EKIVKELYGHAVSE 84

RESULT 68
US-09-457-864-8
; Sequence 8, Application US/09457864
; Patent No. 6455266
; GENERAL INFORMATION:
; APPLICANT: Pioneer HiBred International
; APPLICANT: Bulla, Lee A.
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; FILE REFERENCE: 27112-20037.13
; CURRENT APPLICATION NUMBER: US/09/457,864
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 08/326,117
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mouse
US-09-457-864-8

Query Match 46.9%; Score 38; DB 4; Length 109;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 70 EKIVKELYGHAVSE 84

RESULT 69
US-09-457-865A-8
; Sequence 8, Application US/09457865A
; Patent No. 6613886
; GENERAL INFORMATION:
; APPLICANT: Pioneer HiBred International
; APPLICANT: Bulla, Lee A.
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; FILE REFERENCE: 27112-20037.14
; CURRENT APPLICATION NUMBER: US/09/457,865A
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/178,176
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 08/982,129
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: US 08/326,117
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mouse
US-09-457-865A-8

```
; Sequence 9, Application US/08474067
; Patent No. 5811518
; GENERAL INFORMATION:
; APPLICANT: Ranscht, Barbara
; TITLE OF INVENTION: T-Cadherin Adhesion Molecule
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/474,067
; APPLICATION NUMBER: US/08/474,067
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,361
; FILING DATE: 14-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/607,293
; FILING DATE: 30-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1682
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-474-067-9

Query Match 46.9%; Score 38; DB 2; Length 822;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 168 EKIVKVELYGHAVSE 182

RESULT 73
US-08-474-068A-9
; Sequence 9, Application US/08474068A
; Patent No. 5837525
; GENERAL INFORMATION:
; APPLICANT: Ranscht, Barbara
; TITLE OF INVENTION: T-Cadherin Adhesion Molecule
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,068A

Query Match 46.9%; Score 38; DB 4; Length 109;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 70 EKIVKVELYGHAVSE 84

RESULT 70
US-09-513-999C-5896
; Sequence 5896, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5896
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5896

Query Match 46.9%; Score 38; DB 4; Length 119;
Best Local Similarity 53.3%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 73 QTRAIYDIYKRGLE 87

RESULT 71
US-09-489-039A-7692
; Sequence 7692, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7692
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7692

Query Match 46.9%; Score 38; DB 4; Length 554;
Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 RAAYDQYGHAAFE 15
Db 250 RLGYEYGAAGFQ 262

RESULT 72
US-08-474-067-9
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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,361
; FILING DATE: 14-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/607,293
; FILING DATE: 30-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1686
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-474-068A-9.

Query Match 46.9%; Score 38; DB 2; Length 822;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYGHAAFE 15
:|:|||||
Db 168 EKIVKELYGHAVSE 182

RESULT 74
US-08-472-481-8
; Sequence 8, Application US/08472481
; Patent No. 5863804
; GENERAL INFORMATION:
; APPLICANT: Ranscht, Barbara
; TITLE OF INVENTION: T-Cadherin Adhesion Molecule
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,481
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,361
; FILING DATE: 14-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/607,293
; FILING DATE: 30-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1686
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-472-481-8

Query Match 46.9%; Score 38; DB 2; Length 822;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYGHAAFE 15
:|:|||||
Db 168 EKIVKELYGHAVSE 182

RESULT 75
US-09-513-999C-6016
; Sequence 6016, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6016
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6016

Query Match 45.7%; Score 37; DB 4; Length 75;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYG 10
:|:|||||
Db 61 EKRELYDRYG 70

RESULT 76
US-09-134-000C-5008
; Sequence 5008, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5008
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5008

Query Match 45.7%; Score 37; DB 4; Length 242;
Best Local Similarity 63.6%; Pred. No. 71;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AYDOYGHAAFE 15
:|:|||||
Db 82 AYDOYALKAFQ 92

```
RESULT 77
US-09-248-796A-17629
; Sequence 17629, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17629
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (313), (314), (316), (318), (319)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-17629

Query Match 45.7%; Score 37; DB 4; Length 320;
Best Local Similarity 40.0%; Pred. No. 95;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 67 KORDIYDKYGEAGID 81

RESULT 78
US-09-198-452A-48
; Sequence 48, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 48
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-48

Query Match 45.7%; Score 37; DB 4; Length 392;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 10
DB 58 QKRDSDYDRFG 67

RESULT 79
US-09-438-185A-34
; Sequence 34, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
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; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0032
US-09-438-185A-34

Query Match 45.7%; Score 37; DB 4; Length 406;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 10
DB 72 QKRDSDYDRFG 81

RESULT 80
US-09-134-000C-5523
; Sequence 5523, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5523
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5523

Query Match 45.7%; Score 37; DB 4; Length 434;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
DB 230 KQAOYQQQGVIAFE 243

RESULT 81
US-09-489-039A-10301
; Sequence 10301, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10301
; LENGTH: 556
```

; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10301

Query Match 45.7%; Score 37; DB 4; Length 556;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 AAYDQYGH 11
:|:|:|:|:|
Db 149 ASYFQYGH 156

RESULT 82
US-09-244-805-27

; Sequence 27, Application US/09244805
; Patent No. 6699660

; GENERAL INFORMATION:

; APPLICANT: Worley, Paul F.

; APPLICANT: Lanahan, Anthony

; APPLICANT: Goetz, Bernard

; APPLICANT: Heimisch, Holger

; APPLICANT: Kuner, Rohini

; APPLICANT: Scheek, Sigrid

; APPLICANT: Nikolich, Karoly

; APPLICANT: Zhukovski, Eugene

; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 10496/004001

; CURRENT APPLICATION NUMBER: US/09/244,805

; CURRENT FILING DATE: 1999-02-05

; PRIOR FILING DATE: 60/074,518

; PRIOR FILING DATE: 1998-02-12

; PRIOR APPLICATION NUMBER: 60/074,135

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 27

; LENGTH: 581

; TYPE: PRT

; ORGANISM: Eukaryote

US-09-244-805-27

Query Match 45.7%; Score 37; DB 4; Length 581;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
||| :|:|:|:|
Db 71 KRAPERPGHVAFD 84

RESULT 83

US-09-252-991A-27230

; Sequence 27230, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 27230

; LENGTH: 953

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27230

Query Match 45.7%; Score 37; DB 4; Length 953;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
:|:|:|:|:|
Db 518 RQRAEEQFGHA 529

RESULT 84

US-08-346-849-8

; Sequence 8, Application US/08346849

; Patent No. 5670483

; GENERAL INFORMATION:

; APPLICANT: Zhang, Shuguang

; APPLICANT: Lockshin, Curtis

; APPLICANT: Rich, Alexander

; APPLICANT: Holmes, Todd

; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY

; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES

; TITLE OF INVENTION: THEREFOR

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02173-4799

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/346,849

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/973,326

; FILING DATE: 28 DECEMBER 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Brook, David E.

; REGISTRATION NUMBER: 22,592

; REFERENCE/DOCKET NUMBER: MIT-6008

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 861-6240

; TELEFAX: (617) 861-9540

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 52 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-346-849-8

Query Match 44.4%; Score 36; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYD 7
|||:|:|:|
Db 46 QKRAAYD 52

RESULT 85

US-08-293-284A-8

; Sequence 8, Application US/08293284A

; Patent No. 5955343

; GENERAL INFORMATION:

; APPLICANT: Holmes, Todd

; APPLICANT: Zhang, Shuguang

```
;
; APPLICANT: Rich, Alexander
; APPLICANT: DiPersio, C. Michael
; APPLICANT: Lockshin, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/293,284A
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-9540
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-293-284A-8

Query Match 44.4%; Score 36; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYD 7
Db 46 QKRAAYD 52

RESULT 86
US-08-898-300-8
; Sequence 8, Application US/0898300
; Patent No. 6548630
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/293,284
; FILING DATE: August 22, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/898,300
; FILING DATE: 22 JULY 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,849
; FILING DATE: 30 NOVEMBER 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008FB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-898-300-8

Query Match 44.4%; Score 36; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYD 7
Db 46 QKRAAYD 52

RESULT 87
US-08-824-513-8
; Sequence 8, Application US/08824513
; Patent No. 6800481
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd
; APPLICANT: Zhang, Shuguang
; APPLICANT: Rich, Alexander
; APPLICANT: DiPersio, C. Michael
; APPLICANT: Lockshin, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,513
; FILING DATE: March 26, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/293,284
; FILING DATE: August 22, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
```


; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-824-513-8

Query Match 44.4%; Score 36; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYD 7
Db 46 QKRAAYD 52

RESULT 88
US-09-513-999C-5565
; Sequence 5565, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5565
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5565

Query Match 44.4%; Score 36; DB 4; Length 65;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AAYDQYGHAAF 14
Db 54 AAYDRNGNQAF 64

RESULT 89
US-09-270-767-47445
; Sequence 47445, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47445
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47445

Query Match 44.4%; Score 36; DB 4; Length 130;
Best Local Similarity 46.7%; Pred. No. 55;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAF 15
Db 1 EKDLAYEAGGNAAFQ 15

RESULT 90
US-09-513-999C-6925
; Sequence 6925, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6925
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6925

Query Match 44.4%; Score 36; DB 4; Length 147;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYG 10
Db 138 KRLRYDEYG 146

RESULT 91
US-09-270-767-46278
; Sequence 46278, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46278
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46278

Query Match 44.4%; Score 36; DB 4; Length 152;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYG 10
Db 16 KREVDYKYG 24

RESULT 92
US-09-621-976-5129
; Sequence 5129, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5129
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-5129

Query Match 44.4%; Score 36; DB 4; Length 153;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAA 10
: ||| ||| |||
Db 60 EKRDYDKYG 69

RESULT 93
US-09-270-767-32870
; Sequence 32870, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32870
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32870

Query Match 44.4%; Score 36; DB 4; Length 175;
Best Local Similarity 61.5%; Pred. No. 76;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAA 13
: ||| ||| |||
Db 17 QNOQAKDQYGIAA 29

RESULT 94
US-09-270-767-48087
; Sequence 48087, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48087
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48087

Query Match 44.4%; Score 36; DB 4; Length 175;
Best Local Similarity 61.5%; Pred. No. 76;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAA 13
: ||| ||| |||
Db 17 QNOQAKDQYGIAA 29

RESULT 95

US-09-543-681A-7507
; Sequence 7507, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7507
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7507

Query Match 44.4%; Score 36; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DOYGHA 12
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Db 184 DOYGHA 189

RESULT 96
US-09-248-796A-19977
; Sequence 19977, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19977
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19977

Query Match 44.4%; Score 36; DB 4; Length 330;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGH 10
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Db 25 EKRRYDQFG 34

RESULT 97
US-09-665-479A-8
; Sequence 8, Application US/09665479A
; Patent No. 6673570
; GENERAL INFORMATION:
; APPLICANT: Itoh, Fumiko
; APPLICANT: Itoh, Susumu
; APPLICANT: Heidin, Carl-Henrik

; APPLICANT: ten-Dijke, Peter
; TITLE OF INVENTION: SWAD ASSOCIATING POLYPEPTIDES
; FILE REFERENCE: L00461.70096 US
; CURRENT APPLICATION NUMBER: US/09/665.479A
; CURRENT FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 60/154,846
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-665-479A-8

Query Match 44.4%; Score 36; DB 4; Length 337;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
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Db 59 KKREIYDQFG 68

RESULT 98
US-09-489-039A-10623
; Sequence 10623, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10623
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae

Query Match 44.4%; Score 36; DB 4; Length 387;
Best Local Similarity 53.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAF 14
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Db 266 KRYAFDPQKHAAY 278

RESULT 99
US-09-252-991A-26237
; Sequence 26237, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26237
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26237

Query Match 44.4%; Score 36; DB 4; Length 412;
Best Local Similarity 46.7%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
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Db 29 QRRVAHQAGQAVLE 43

RESULT 100

US-09-252-991A-21980
; Sequence 21980, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21980
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21980

Query Match 44.4%; Score 36; DB 4; Length 487;
Best Local Similarity 72.7%; Pred. No. 2.2e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAYDQYGHAAF 14
:|:|:|:|:|:
Db 39 AAPDQFGIAAF 49

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Job time : 24 secs

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18: /cgn2_6/ptodata/2/pubpaa/US10A_NEW_PUB.pep:*					
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1	81	100.0	15 9	US-09-756-983-10	Sequence 10, Appl
2	81	100.0	15 9	US-09-828-574-10	Sequence 10, Appl
3	81	100.0	15 14	US-10-001-938-27	Sequence 27, Appl
4	81	100.0	15 14	US-10-299-540-4	Sequence 4, Appl
5	81	100.0	15 14	US-10-299-184-4	Sequence 4, Appl
6	81	100.0	15 14	US-10-239-313A-444	Sequence 444, Appl
7	81	100.0	15 16	US-10-614-639A-10	Sequence 10, Appl
8	81	100.0	15 17	US-10-614-414A-10	Sequence 10, Appl
9	81	100.0	16 14	US-10-001-938-3	Sequence 3, Appl
10	81	100.0	16 14	US-10-239-313A-447	Sequence 447, Appl
11	81	100.0	340 9	US-09-764-868-1153	Sequence 1153, Ap
341	100.0	9	US-09-764-868-1152	Sequence 1152, Ap	
376	15	US-10-369-493-689	Sequence 689, App		
378	15	US-10-369-493-386	Sequence 386, App		
378	15	US-10-369-493-21305	Sequence 21305, A		
365	15	US-10-369-493-10648	Sequence 10648, A		
376	15	US-10-369-493-12087	Sequence 12087, A		
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23	67	82.7	376	16	US-10-375-010-22
24	67	82.7	379	15	US-10-368-493-7330
25	67	82.7	380	15	US-10-369-493-4573
26	63	77.8	376	15	US-10-369-493-47
27	62	76.5	374	15	US-10-369-493-13658
28	61	75.3	378	15	US-10-369-493-8450
29	60	74.1	375	15	US-10-369-493-15859
30	60	74.1	376	15	US-10-369-493-15487
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35	56	69.1	362	15	US-10-369-493-9305
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43	52	64.2	360	15	US-10-369-493-10371
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48	50	61.7	297	15	US-10-282-122A-54551
49	50	61.7	362	16	US-10-437-963-190831
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55	49	60.5	158	15	US-10-425-114-48912
56	49	60.5	228	16	US-10-767-701-40388
57	49	60.5	311	15	US-10-424-599-144051
58	49	60.5	326	16	US-10-425-115-300448
59	49	60.5	370	15	US-10-369-493-17209
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62	49	60.5	542	16	US-10-437-963-123435
63	48	59.3	423	15	US-10-369-493-12619
64	47	58.0	511	15	US-10-369-493-21871
65	46	56.8	116	15	US-10-424-599-233524
66	46	56.8	135	16	US-10-425-115-295592
67	46	56.8	192	15	US-10-424-599-237535
68	46	56.8	217	15	US-10-424-599-257471
69	46	56.8	352	16	US-10-739-930-7746
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85 45 55.6 822 18 US-10-756-149-5816 Sequence 5816, Ap
86 44 54.3 59 16 US-10-425-115-337846 Sequence 337846,
87 44 54.3 94 16 US-10-425-115-341282 Sequence 341282,
88 44 54.3 103 16 US-10-425-115-205457 Sequence 205457,
89 44 54.3 168 16 US-10-767-701-57856 Sequence 57856, A
90 44 54.3 173 16 US-10-425-115-197095 Sequence 197095,
91 44 54.3 183 16 US-10-425-115-295514 Sequence 295514,
92 44 54.3 192 16 US-10-425-115-295500 Sequence 295500,
93 44 54.3 194 16 US-10-425-115-295516 Sequence 295516,
94 44 54.3 211 16 US-10-767-701-47401 Sequence 47401, A
95 44 54.3 212 16 US-10-425-115-309309 Sequence 309309,
96 44 54.3 217 15 US-10-424-599-271036 Sequence 271036,
97 44 54.3 244 16 US-10-425-115-217751 Sequence 217751,
98 44 54.3 273 16 US-10-437-963-157461 Sequence 157461,
99 44 54.3 352 14 US-10-077-584-8 Sequence 8, Appli
100 44 54.3 363 16 US-10-425-115-304214 Sequence 304214,
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ALIGNMENTS

RESULT 1

US-09-756-983-10

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; Sequence 10, Application US/09756983
; Patent No. US20020122818A1
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJpl heat shock protein
US-09-756-983-10
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Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 QKRAAYDQYGHAAFE 15
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RESULT 2

US-09-828-574-10

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; Sequence 10, Application US/09828574
; Patent No. US20020146759A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: PRAKKEN, Berent J.
; TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: UCSD1310-1
; CURRENT APPLICATION NUMBER: US/09/828,574
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/224,104
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 13
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: dnaJpl peptide
US-09-828-574-10
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Query Match 100.0%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 QKRAAYDQYGHAAFE 15
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RESULT 3

US-10-001-938-27

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; Sequence 27, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Escherichia coli
; OTHER INFORMATION:
US-10-001-938-27
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Query Match 100.0%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 QKRAAYDQYGHAAFE 15
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RESULT 4

US-10-299-540-4

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; Sequence 4, Application US/10299540
; Publication No. US20030143238A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTEC
; TITLE OF INVENTION: AGAINST ARTHRITIS
; FILE REFERENCE: UCSD1370-7
; CURRENT APPLICATION NUMBER: US/10/299,540
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
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; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic dnaJp1
US-10-299-540-4

Query Match 100.0%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15
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RESULT 5

US-10-299-184-4
; Sequence 4, Application US/10299184
; Publication No. US20030147910A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore

; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION
; TITLE OF INVENTION: AGAINST ARTHRITIS
; FILE REFERENCE: UCSD1370-6
; CURRENT APPLICATION NUMBER: US/10/299,184
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic dnaJp1
US-10-299-184-4

Query Match 100.0%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15
Db 1 OKRAAYDOYGHAAFE 15

RESULT 6

US-10-239-313A-444
; Sequence 444, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane

; TITLE OF INVENTION: MOLECULES OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID

; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-444

Query Match 100.0%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15
Db 1 OKRAAYDOYGHAAFE 15

RESULT 7

US-10-614-639A-10
; Sequence 10, Application US/10614639A
; Publication No. US20040224009A1
; GENERAL INFORMATION:
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION
; TITLE OF INVENTION: AND MODULATION OF ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: AND-TCCIP1-DIV2
; CURRENT APPLICATION NUMBER: US/10/614,639A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: 09/756,983
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/US99/24666
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-614-639A-10

Query Match 100.0%; Score 81; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15
Db 1 OKRAAYDOYGHAAFE 15

RESULT 8

US-10-614-414A-10
; Sequence 10, Application US/10614414A
; Publication No. US20050079208A1
; GENERAL INFORMATION:
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION
; TITLE OF INVENTION: AND MODULATION OF ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: AND-TCCIP1-DIV1
; CURRENT APPLICATION NUMBER: US/10/614,414A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: 09/756,983
; PRIOR FILING DATE: 2001-01-09

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; PRIOR APPLICATION NUMBER: PCT/US99/24666
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-614-414A-10

Query Match          100.0%; Score 81; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 9
US-10-001-938-3
; Sequence 3, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-001-938-3

Query Match          100.0%; Score 81; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 10
US-10-239-313A-447
; Sequence 447, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/037111

; PRIOR APPLICATION NUMBER: PCT/US99/24666
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-447

Query Match          100.0%; Score 81; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 11
US-09-764-868-1153
; Sequence 1153, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1153
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (110)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (135)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (156)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (196)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (216)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1153

Query Match          100.0%; Score 81; DB 9; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 25 QKRAAYDQYGHAAFE 39

RESULT 12
US-09-764-868-1152
; Sequence 1152, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```


; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1152
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-1152

Query Match 100.0%; Score 81; DB 9; Length 341;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 26 QKRAAYDQYGHAAFE 40
|||||

RESULT 13

US-10-369-493-689
; Sequence 689, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 689
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-369-493-689

Query Match 100.0%; Score 81; DB 15; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75
|||||

RESULT 14

US-10-369-493-386
; Sequence 386, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 386
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-386

Query Match 100.0%; Score 81; DB 15; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75
|||||

RESULT 15

US-10-369-493-21305
; Sequence 21305, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21305
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-21305

Query Match 100.0%; Score 81; DB 15; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75
|||||

RESULT 16

US-10-369-493-10648
; Sequence 10648, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10648
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Shingomonas aromaticivorans
US-10-369-493-10648

Query Match 91.4%; Score 74; DB 15; Length 365;

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Best Local Similarity 86.7%; Pred. No. 0.00023; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 0;

QY 1 OKRAAYDQYGHAAFE 15
Db 56 OKRAAYDRYGHAAQF 70

RESULT 17
US-10-369-493-12087
; Sequence 12087, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12087
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-12087

Query Match 90.1%; Score 73; DB 15; Length 376;
Best Local Similarity 86.7%; Pred. No. 0.00035; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 0;

QY 1 OKRAAYDQYGHAAFE 15
Db 60 OKRAAYDRYGHAAFE 74

RESULT 18
US-09-828-574-11
; Sequence 11, Application US/09828574
; Patent No. US20020146759A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: PRAKSEN, Berent J.
; TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: UCSD1310-1
; CURRENT APPLICATION NUMBER: US/09/828,574
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/224,104
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Irrelevant dnaJpV peptide
US-09-828-574-11

Query Match 88.9%; Score 72; DB 9; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.9e-05; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 0;

QY 2 KRAAYDQYGHAAFE 15
Db 2 ERAAYDQYGHAAFE 15

RESULT 19
US-10-299-540-5
; Sequence 5, Application US/10299540
; Publication No. US20030143238A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTEC
; FILE REFERENCE: UCSD1370-7
; CURRENT APPLICATION NUMBER: US/10/299,540
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant dnaJ peptide
US-10-299-540-5

Query Match 88.9%; Score 72; DB 14; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.9e-05; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 0;

QY 2 KRAAYDQYGHAAFE 15
Db 2 ERAAYDQYGHAAFE 15

RESULT 20
US-10-299-184-5
; Sequence 5, Application US/10299184
; Publication No. US20030147910A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTEC
; FILE REFERENCE: UCSD1370-6
; CURRENT APPLICATION NUMBER: US/10/299,184
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant dnaJ peptide
US-10-299-184-5
```

Query Match 88.9%; Score 72; DB 14; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.9e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
:|||||:|||||
DB 2 ERAAYDQYGHAAFE 15

RESULT 21
US-10-369-493-8065
; Sequence 8065, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8065
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-8065

Query Match 85.2%; Score 69; DB 15; Length 382;
Best Local Similarity 85.7%; Pred. No. 0.0017;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
:|||||:|||||
DB 62 KKAAYDRYGHAAFE 75

RESULT 22
US-10-369-493-21849
; Sequence 21849, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21849
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Rhodobacter capsulatus
US-10-369-493-21849

Query Match 85.2%; Score 69; DB 15; Length 384;
Best Local Similarity 85.7%; Pred. No. 0.0018;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
:|||||:|||||

Db 62 KKAAYDRYGHAAFE 75

RESULT 23

US-10-375-010-22
; Sequence 22, Application US/10375010
; Publication No. US20040170985A1
; GENERAL INFORMATION:
; APPLICANT: USUDA, Yoshihiro
; APPLICANT: NISHIO, Yosuke
; APPLICANT: YASUEDA, Hisashi
; APPLICANT: SUGIMOTO, Shinichi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING POLYPEPTIDES INVOLVED IN THE STRESS RES
; FILE REFERENCE: 232744US0
; CURRENT APPLICATION NUMBER: US/10/375,010
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Methylophilus methylotrophus
US-10-375-010-22

Query Match 82.7%; Score 67; DB 16; Length 376;
Best Local Similarity 80.0%; Pred. No. 0.0038;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
:|||||:|||||
DB 63 QKRAAYDQYGHAGVD 77

RESULT 24

US-10-369-493-7330
; Sequence 7330, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7330
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7330

Query Match 82.7%; Score 67; DB 15; Length 379;
Best Local Similarity 80.0%; Pred. No. 0.0038;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
:|||||:|||||
DB 61 QKRAAYDQYGHAGVD 75

RESULT 25

US-10-369-493-4573
; Sequence 4573, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei

```
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4573
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4573

Query Match      82.7%; Score 67; DB 15; Length 380;
Best Local Similarity 80.0%; Pred. No. 0.0038;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
Db 61 OKRAAYDQYGHAGVD 75

RESULT 26
US-10-369-493-47
; Sequence 47, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 47
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Aquifex aeolicus
US-10-369-493-47

Query Match      77.8%; Score 63; DB 15; Length 376;
Best Local Similarity 73.3%; Pred. No. 0.019;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
Db 63 EKRLYDQYGHAAFE 77

RESULT 27
US-10-369-493-13658
; Sequence 13658, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
```

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; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13658
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13658

Query Match      76.5%; Score 62; DB 15; Length 374;
Best Local Similarity 78.6%; Pred. No. 0.027;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db 62 KRAAYDQYGHAGVD 75

RESULT 28
US-10-369-493-8450
; Sequence 8450, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8450
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Ralstonia metallidurans
US-10-369-493-8450

Query Match      75.3%; Score 61; DB 15; Length 378;
Best Local Similarity 66.7%; Pred. No. 0.041;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
Db 61 EKRAAYDQYGHAGVD 75

RESULT 29
US-10-369-493-15859
; Sequence 15859, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15859
; LENGTH: 375
```

; TYPE: PRT
; ORGANISM: Xanthomonas campestris
US-10-369-493-15859

Query Match 74.1%; Score 60; DB 15; Length 375;
Best Local Similarity 78.6%; Pred. No. 0.061;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15
Db 62 KRAYDAHGHAFFE 75

RESULT 30

US-10-369-493-15487
; Sequence 15487, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15487

; LENGTH: 376
; TYPE: PRT

; ORGANISM: Xanthomonas campestris
US-10-369-493-15487

Query Match 74.1%; Score 60; DB 15; Length 376;
Best Local Similarity 78.6%; Pred. No. 0.061;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15
Db 62 KRAYDAHGHAFFE 75

RESULT 31

US-10-369-493-9641
; Sequence 9641, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9641

; LENGTH: 358
; TYPE: PRT

; ORGANISM: Desulfitobacterium hafnense
US-10-369-493-9641

Query Match 72.8%; Score 59; DB 15; Length 358;
Best Local Similarity 66.7%; Pred. No. 0.086;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
Db 46 EKRAYDQMGHSAFD 60

RESULT 32

US-10-369-493-18523
; Sequence 18523, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18523

; LENGTH: 379
; TYPE: PRT

; ORGANISM: Lactococcus lactis
US-10-369-493-18523

Query Match 71.6%; Score 58; DB 15; Length 379;
Best Local Similarity 91.7%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHGA 12
Db 60 OKRAAYDQYGEA 71

RESULT 33

US-10-369-493-16754
; Sequence 16754, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16754

; LENGTH: 385
; TYPE: PRT

; ORGANISM: Caulobacter crescentus
US-10-369-493-16754

Query Match 71.6%; Score 58; DB 15; Length 385;
Best Local Similarity 83.3%; Pred. No. 0.14;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHGA 12
Db 59 OKRAAYDREGHA 70

RESULT 34

```
US-10-369-493-19646
; Sequence 19646, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19646
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Nitrosomonas europaea
US-10-369-493-19646
Query Match 70.4%; Score 57; DB 15; Length 369;
Best Local Similarity 90.9%; Pred. No. 0.2;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGH 12
|||||:||||
Db 62 KRAAYDQYGH 72

RESULT 35
US-10-369-493-9305
; Sequence 9305, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9305
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-10-369-493-9305
Query Match 69.1%; Score 56; DB 15; Length 362;
Best Local Similarity 66.7%; Pred. No. 0.29;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
:|:|:|:|:|:|
Db 61 KKRKLYDTHGHAPE 75

RESULT 36
US-10-474-776-634
; Sequence 634, Application US/10474776
; Publication No. US20040110181A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYH
; TITLE OF INVENTION: ANTIGENS AND USES THEREOF
```

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; FILE REFERENCE: AM100649-PCT
; CURRENT APPLICATION NUMBER: US/10/474,776
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 634
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-474-776-634
Query Match 69.1%; Score 56; DB 16; Length 378;
Best Local Similarity 91.7%; Pred. No. 0.3;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
|||||:|||||
Db 60 QKRAAYDQYGAA 71

RESULT 37
US-10-472-928-900
; Sequence 900, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926W0
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 900
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: dnaJ protein (dnaJ)
; OTHER INFORMATION: Cellular location: cytoplasm
; OTHER INFORMATION: Similar to strain R6 sequence 15902500 (0.E+01.)
US-10-472-928-900
Query Match 69.1%; Score 56; DB 17; Length 378;
Best Local Similarity 91.7%; Pred. No. 0.3;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
|||||:|||||
Db 60 QKRAAYDQYGAA 71

RESULT 38
US-10-617-320-3487
; Sequence 3487, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
```

COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3487:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...379
SEQUENCE DESCRIPTION: SEQ ID NO: 3487:
US-10-617-320-3487

Query Match 69.1%; Score 56; DB 18; Length 379;
Best Local Similarity 91.7%; Pred. No. 0.3;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
DB 61 QKRAAYDQYGAA 72

RESULT 39
US-09-861-451A-2
Sequence 2, Application US/09861451A
Patent No. US20020068289A1
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific & Industrial Research Orga
TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences
FILE REFERENCE: FP34033/01
CURRENT APPLICATION NUMBER: US/09/861,451A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: PP7273
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 368
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Deduced protein
OTHER INFORMATION: sequence from clone PAD612
US-09-861-451A-2

Query Match 67.9%; Score 55; DB 9; Length 368;
Best Local Similarity 64.3%; Pred. No. 0.43;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
|||:::|||||

Db 67 KRKYDKFGHAAFD 80
RESULT 40
US-10-299-540-6
Sequence 6, Application US/10299540
Publication No. US20030143238A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: CARSON, Dennis A.
APPLICANT: ALBANI, Salvatore
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTE
TITLE OF INVENTION: AGAINST ARTHRITIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF
TITLE OF INVENTION: ARTHRITIS
FILE REFERENCE: UCSD1370-7
CURRENT APPLICATION NUMBER: US/10/299,540
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 09/616,247
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/107,615
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 08/618,464
PRIOR FILING DATE: 1996-03-15
PRIOR APPLICATION NUMBER: US 08/246,988
PRIOR FILING DATE: 1994-05-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Bacterial dnaUp2 peptide
US-10-299-540-6

Query Match 66.7%; Score 54; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
DB 6 QKRAAYDQYG 15
|||||

RESULT 41
US-10-299-184-6
Sequence 6, Application US/10299184
Publication No. US20030147910A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: CARSON, Dennis A.
APPLICANT: ALBANI, Salvatore
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTE
TITLE OF INVENTION: AGAINST ARTHRITIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF
TITLE OF INVENTION: ARTHRITIS
FILE REFERENCE: UCSD1370-6
CURRENT APPLICATION NUMBER: US/10/299,184
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: US 09/616,247
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/107,615
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 08/618,464
PRIOR FILING DATE: 1996-03-15
PRIOR APPLICATION NUMBER: US 08/246,988
PRIOR FILING DATE: 1994-05-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:

; OTHER INFORMATION: Bacterial dnaJp2 peptide
US-10-299-184-6

Query Match 66.7%; Score 54; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQVG 10
Db 6 QKRAAYDQVG 15
|||||

RESULT 42
US-10-425-115-239397
; Sequence 239397, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 239397
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_149916C.1.pep
US-10-425-115-239397

Query Match 66.7%; Score 54; DB 16; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQVG 10
Db 43 QKRAAYDQVG 52
|||||

RESULT 43
US-10-369-493-10371
; Sequence 10371, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10371
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Cytophaga hutchinsonii
US-10-369-493-10371

Query Match 64.2%; Score 52; DB 15; Length 360;
Best Local Similarity 69.2%; Pred. No. 1.4;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQVGHAA 13

Db 59 EKRRYDQYGHQA 71
:|||

RESULT 44
US-10-369-493-23206
; Sequence 23206, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23206
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23206

Query Match 64.2%; Score 52; DB 15; Length 372;
Best Local Similarity 81.8%; Pred. No. 1.4;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11
Db 60 QKRAHYDQFGH 70
|||||

RESULT 45
US-10-369-493-1212
; Sequence 1212, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1212
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Methanobacterium thermoautotrophicum
US-10-369-493-1212

Query Match 64.2%; Score 52; DB 15; Length 376;
Best Local Similarity 53.3%; Pred. No. 1.4;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15
Db 60 EKRAHYDQFGHAGMD 74
:|||

RESULT 46
US-10-767-701-40315
; Sequence 40315, Application US/10767701

Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 40315
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C6829_1.pep
US-10-767-701-40315

Query Match 61.7%; Score 50; DB 16; Length 175;
Best Local Similarity 90.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
|||||
Db 61 QKRAVYDQYG 70

RESULT 47

US-10-425-115-289174
; Sequence 289174, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 289174
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_26817C.1.pep
US-10-425-115-289174

Query Match 61.7%; Score 50; DB 16; Length 241;
Best Local Similarity 90.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
|||||
Db 61 QKRAVYDQYG 70

RESULT 48

US-10-282-122A-54551
; Sequence 54551, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John

APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54551
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-282-122A-54551

Query Match 61.7%; Score 50; DB 15; Length 297;
Best Local Similarity 64.3%; Pred. No. 2.5;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAF 14
:|||||
Db 58 KKRAQYDQYGDMSF 71

RESULT 49

US-10-437-963-190831
; Sequence 190831, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 190831
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87208C.1.pep
US-10-437-963-190831

```
Query Match      61.7%; Score 50; DB 16; Length 362;
Best Local Similarity 90.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
      ||||| |||||
Db      61 QGRAVDQYG 70

RESULT 50
US-10-425-115-289176
; Sequence 289176, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 289176
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_26819C.1.pep
US-10-425-115-289176

Query Match      61.7%; Score 50; DB 16; Length 362;
Best Local Similarity 90.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
      ||||| |||||
Db      61 QGRAVDQYG 70

RESULT 51
US-10-437-963-108162
; Sequence 108162, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 108162
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_12442C.1.pep
US-10-437-963-108162

Query Match      61.7%; Score 50; DB 16; Length 383;
Best Local Similarity 90.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
```

```
      ||||| |||||
Db      95 QGRAVDQYG 104

RESULT 52
US-10-425-114-59964
; Sequence 59964, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59964
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-244-F10_FLI.pep
US-10-425-114-59964

Query Match      61.7%; Score 50; DB 15; Length 404;
Best Local Similarity 90.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
      ||||| |||||
Db      103 QGRAVDQYG 112

RESULT 53
US-10-424-599-191916
; Sequence 191916, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191916
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1531C.1.pep
US-10-424-599-191916

Query Match      60.5%; Score 49; DB 15; Length 146;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
      ||||| |||||
Db      61 QGRAVDQYG 70

RESULT 54
US-10-425-115-206200
; Sequence 206200, Application US/10425115
```

Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 206200
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(150)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_119639C.1.pep
US-10-425-115-206200

Query Match 60.5%; Score 49; DB 16; Length 150;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
Db 98 QKRAAYDQYGEA 109

RESULT 55

US-10-425-114-48912
; Sequence 48912, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 48912
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3067-017-D1_Flt.pep
US-10-425-114-48912

Query Match 60.5%; Score 49; DB 15; Length 158;
Best Local Similarity 90.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 10
Db 65 QKRAAYDQYGH 74

RESULT 56

US-10-767-701-40388
; Sequence 40388, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 40388
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C58008_1.pep
US-10-767-701-40388

Query Match 60.5%; Score 49; DB 16; Length 228;
Best Local Similarity 75.0%; Pred. No. 2.9;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
Db 131 QKRAAYDQYGEA 142

RESULT 57

US-10-424-599-144051
; Sequence 144051, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 144051
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(311)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101090C.1.pep
US-10-424-599-144051

Query Match 60.5%; Score 49; DB 15; Length 311;
Best Local Similarity 75.0%; Pred. No. 3.9;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
Db 120 QKRAAYDQYGEA 131

RESULT 58

US-10-425-115-300448
; Sequence 300448, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 300448
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_37079C.1.pep
US-10-425-115-300448

Query Match 60.5%; Score 49; DB 16; Length 326;
Best Local Similarity 90.0%; Pred. No. 4.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
Db 59 QKRAAYDQYG 68

RESULT 59

US-10-369-493-17209
; Sequence 17209, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17209
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-369-493-17209

Query Match 60.5%; Score 49; DB 15; Length 370;
Best Local Similarity 72.7%; Pred. No. 4.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 11
Db 60 QKRAHYDQFGH 70

RESULT 60

US-10-424-599-249417
; Sequence 249417, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 249417
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_37079C.1.pep

; NAME/KEY: unsure
; LOCATION: (1)..(485)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_67253C.1.pep
US-10-424-599-249417

Query Match 60.5%; Score 49; DB 15; Length 485;
Best Local Similarity 75.0%; Pred. No. 6.2;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
Db 123 KKRALYDQYGEA 134

RESULT 61

US-10-425-115-348539
; Sequence 348539, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 348539
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_81031C.1.pep
US-10-425-115-348539

Query Match 60.5%; Score 49; DB 16; Length 487;
Best Local Similarity 75.0%; Pred. No. 6.2;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
Db 122 KKRALYDQYGEA 133

RESULT 62

US-10-437-963-123435
; Sequence 123435, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 123435
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_26270C.1.pep

US-10-437-963-123435

Query Match 60.5%; Score 49; DB 16; Length 542;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
Db 181 KKRALYDQYGEA 192

RESULT 63

US-10-369-493-12619

; Sequence 12619, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 12619

; LENGTH: 423

; TYPE: PRT

; ORGANISM: Aspergillus nidulans

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)...(423)

; OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-12619

Query Match 59.3%; Score 48; DB 15; Length 423;
Best Local Similarity 53.3%; Pred. No. 8;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
Db 138 KKRETYDRFGSAAPD 152

RESULT 64

US-10-369-493-21871

; Sequence 21871, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 21871

; LENGTH: 511

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-10-369-493-21871

Query Match 58.0%; Score 47; DB 15; Length 511;

Best Local Similarity 69.2%; Pred. No. 14;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAAF 14
Db 117 KRQYDQFGPAAF 129

RESULT 65

US-10-424-599-233524

; Sequence 233524, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovalic, David K

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 233524

; LENGTH: 116

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_52899C.1.pap

US-10-424-599-233524

Query Match 56.8%; Score 46; DB 15; Length 116;
Best Local Similarity 80.0%; Pred. No. 4.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
Db 61 QKRAIYDEYG 70

RESULT 66

US-10-425-115-295592

; Sequence 295592, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 295592

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)...(135)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_32659C.1.pap

US-10-425-115-295592

Query Match 56.8%; Score 46; DB 16; Length 135;
Best Local Similarity 60.0%; Pred. No. 5.5;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
||| ||||| |;

```
Db 65 QKREYDQYGDALK 79
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7746
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C251922_1.p
US-10-739-930-7746
Query Match 56.8%; Score 46; DB 16; Length 352;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
   :||| |||||
Db 73 EKRAIYDQYG 82

RESULT 70
US-10-739-930-7078
; Sequence 7078, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7078
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(382)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: BRANA-23APR03-C508_15.p
US-10-739-930-7078
Query Match 56.8%; Score 46; DB 16; Length 382;
Best Local Similarity 53.3%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
   :||| |||||
Db 36 QRRATYGNYSNAAFQ 50

RESULT 71
US-10-493-3465
; Sequence 3465, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21

Db 65 QKREYDQYGDALK 79
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 237535
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56519C.1.p
US-10-424-599-237535
Query Match 56.8%; Score 46; DB 15; Length 192;
Best Local Similarity 80.0%; Pred. No. 7.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
   ||| |||||
Db 61 QKRGVYDQYG 70

RESULT 68
US-10-424-599-257471
; Sequence 257471, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 257471
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7451C.1.p
US-10-424-599-257471
Query Match 56.8%; Score 46; DB 15; Length 217;
Best Local Similarity 80.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
   ||| |||||
Db 61 QKRGVYDQYG 70

RESULT 69
US-10-739-930-7746
; Sequence 7746, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
```

; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3465
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-3465

Query Match 56.8%; Score 46; DB 15; Length 401;
Best Local Similarity 53.3%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAPE 15
Db 68 EKRFQDFGGAAGPE 82

RESULT 72

US-10-424-599-282287
; Sequence 282287, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 282287
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_96928C.1.pep
US-10-424-599-282287

Query Match 56.8%; Score 46; DB 15; Length 427;
Best Local Similarity 57.1%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAAF 14
Db 145 EKRFQDQVGHDAY 158

RESULT 73

US-10-425-115-337892
; Sequence 337892, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 337892
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(115)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_71325C.1.pep

US-10-425-115-337892

Query Match 55.6%; Score 45; DB 16; Length 115;
Best Local Similarity 80.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGH 10
Db 62 OKRTIYDQYGH 71

RESULT 74

US-10-425-114-72263
; Sequence 72263, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72263
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE034C01_FLI.ppe
US-10-425-114-72263

Query Match 55.6%; Score 45; DB 15; Length 133;
Best Local Similarity 63.6%; Pred. No. 8;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGH 11
Db 98 QORVEYDRYGH 108

RESULT 75

US-10-424-599-257493
; Sequence 257493, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 257493
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7453C.1.pep
US-10-424-599-257493

Query Match 55.6%; Score 45; DB 15; Length 153;
Best Local Similarity 80.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGH 10

Db 61 QKRGYDQYG 70
||| |||||

RESULT 76

US-09-833-245-652
; Sequence 652, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 652
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (204)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (305)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-652

Query Match 55.6%; Score 45; DB 11; Length 332;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
: |||: |||||
Db 84 EKRSYDQYGD 95

RESULT 77

US-10-425-115-360745
; Sequence 360745, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 360745
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(340)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_92181C.1.p
US-10-425-115-360745

Query Match 55.6%; Score 45; DB 16; Length 340;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRAAYDQYG 10
||| |||||
Db 63 KRAVYDQYG 71

RESULT 78

US-10-437-963-126854
; Sequence 126854, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 126854
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_29360C.1.p
US-10-437-963-126854

Query Match 55.6%; Score 45; DB 16; Length 342;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
||| |||||
Db 62 QKRAVYDQYG 71

RESULT 79

US-10-739-930-6016
; Sequence 6016, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6016
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: ARATH-23APR03-C207692_1.p
US-10-739-930-6016

Query Match 55.6%; Score 45; DB 16; Length 346;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYG 10
||| |||||
Db 63 KRAAYDQYG 71

RESULT 80
US-10-425-114-37469
; Sequence 37469, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37469
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-004-A3_FLI.pep
US-10-425-114-37469

Query Match 55.6%; Score 45; DB 15; Length 352;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRAAYDQYG 10
||| |||||
DB 74 KRAVDQYG 82

RESULT 81
US-10-437-963-126176
; Sequence 126176, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 126176
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_28749C.1.pep
US-10-437-963-126176

Query Match 55.6%; Score 45; DB 16; Length 356;
Best Local Similarity 80.0%; Pred. No. 22;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
||| |||||
DB 60 QKRAVDQFG 69

RESULT 82

US-10-104-047-2714
; Sequence 2714, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2714
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2714

Query Match 55.6%; Score 45; DB 15; Length 595;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
: ||| : |||||
DB 84 EKRSNYDQYGDA 95

RESULT 83
US-10-322-281-574
; Sequence 574, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 574
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-574

Query Match 55.6%; Score 45; DB 16; Length 696;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
: ||| : |||||
DB 6 EKRSNYDQYGDA 17

RESULT 84
US-09-833-245-653
; Sequence 653, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 653
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-653

Query Match      55.6%; Score 45; DB 11; Length 737;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 OKRAAYDQYCHA 12
      :||: |||||
Db      84 EKRSNYDQYGA 95

RESULT 85
US-10-756-149-5816
; Sequence 5816, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5816
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5816

Query Match      55.6%; Score 45; DB 18; Length 822;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 OKRAAYDQYCHA 12
      :||: |||||
Db      124 EKRSNYDQYGA 135

RESULT 86
US-10-425-115-337846
; Sequence 337846, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 337846
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_71284C.1.pep
US-10-425-115-337846

Query Match      54.3%; Score 44; DB 16; Length 59;
Best Local Similarity 53.3%; Pred. No. 5.2;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 OKRAAYDQYCHAAFE 15
      :||: |||||

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 653
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-653

Query Match      55.6%; Score 45; DB 11; Length 737;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 OKRAAYDQYCHA 12
      :||: |||||
Db      84 EKRSNYDQYGA 95

RESULT 87
US-10-425-115-341282
; Sequence 341282, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 341282
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(94)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_74415C.1.pep
US-10-425-115-341282

Query Match      54.3%; Score 44; DB 16; Length 94;
Best Local Similarity 61.5%; Pred. No. 8.3;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 OKRAAYDQYGHAA 13
      :||: |||||
Db      54 EKRIYDQYGEDA 66

RESULT 88
US-10-425-115-205457
; Sequence 205457, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 205457
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(103)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_118964C.1.pep
US-10-425-115-205457

Query Match      54.3%; Score 44; DB 16; Length 103;
Best Local Similarity 53.3%; Pred. No. 9.2;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 OKRAAYDQYGHAAFE 15
      :||: |||||
```

Db 79 EKREIYDQYGEDALK 93

RESULT 89

US-10-767-701-57856

; Sequence 57856, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 57856

; LENGTH: 168

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE:

; OTHER INFORMATION: Clone ID: 30973076.pep

US-10-767-701-57856

Query Match

Best Local Similarity 54.3%; Score 44; DB 16; Length 168;

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

:||:|||||:

Db 7 EKRSIYDKYGEAGLK 21

RESULT 90

US-10-425-115-197095

; Sequence 197095, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 197095

; LENGTH: 173

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(173)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_111333C.1.pep

US-10-425-115-197095

Query Match

Best Local Similarity 54.3%; Score 44; DB 16; Length 173;

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

:||:|||||:

Db 131 EKRSIYDKYGEAGLK 145

RESULT 91

US-10-425-115-295514

; Sequence 295514, Application -US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 295514

; LENGTH: 183

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(183)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_32589C.1.pep

US-10-425-115-295514

Query Match

Best Local Similarity 54.3%; Score 44; DB 16; Length 183;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

:||:|||||:

Db 65 EKREIYDQYGEDALK 79

RESULT 92

US-10-425-115-295500

; Sequence 295500, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 295500

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(192)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_32576C.1.pep

US-10-425-115-295500

Query Match

Best Local Similarity 54.3%; Score 44; DB 16; Length 192;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

:||:|||||:

Db 65 EKREIYDQYGEDALK 79

RESULT 93

US-10-425-115-295516

; Sequence 295516, Application US/10425115

; Publication No. US20040214272A1

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; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 295516
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Zea mays
; NAME/KEY: unsure
; LOCATION: (1)..(194)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRP4577_32590C.1.pep
US-10-425-115-295516

Query Match      54.3%; Score 44; DB 16; Length 194;
Best Local Similarity 53.3%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
   :||| ||||| | :
Db 65 EKREIYDQYGEDALK 79

RESULT 94
US-10-767-701-47401
; Sequence 47401, Application US/107677701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 47401
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(211)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C3435_5.pep
US-10-767-701-47401

Query Match      54.3%; Score 44; DB 16; Length 211;
Best Local Similarity 53.3%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
   :||| ||||| | :
Db 65 EKREIYDQYGEDALK 79

RESULT 95
US-10-425-115-309309
; Sequence 309309, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
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; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 309309
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Zea mays
; NAME/KEY: unsure
; LOCATION: (1)..(212)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRP4577_45155C.1.pep
US-10-425-115-309309

Query Match      54.3%; Score 44; DB 16; Length 212;
Best Local Similarity 53.3%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
   :||| ||||| | :
Db 66 EKREIYDQYGEDALK 80

RESULT 96
US-10-424-599-271036
; Sequence 271036, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 271036
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_86764C.1.pep
US-10-424-599-271036

Query Match      54.3%; Score 44; DB 15; Length 217;
Best Local Similarity 53.3%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
   :||| ||||| | :
Db 65 EKREIYDQYGEDALK 79

RESULT 97
US-10-425-115-217751
; Sequence 217751, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
```

; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 217751
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(244)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_130186C.1.pep
US-10-425-115-217751

Query Match 54.3%; Score 44; DB 16; Length 244;
Best Local Similarity 53.3%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 66 EKREIYDQYGEDAIK 80

RESULT 98

US-10-437-963-157461
; Sequence 157461, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 157461
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_5702C.1.pep
US-10-437-963-157461

Query Match 54.3%; Score 44; DB 16; Length 273;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRAAYDQYG 10
Db 63 KRALYDQYG 71

RESULT 99

US-10-077-584-8
; Sequence 8, Application US/10077584
; Publication No. US20030073610A1
; GENERAL INFORMATION:
; APPLICANT: LINDQUIST, SUSAN
; APPLICANT: KROBITSCH, SYLVIA
; APPLICANT: OUTEIRO, TIAGO F.
; TITLE OF INVENTION: YEAST SCREENS FOR THE TREATMENT OF HUMAN DISEASE
; FILE REFERENCE: ARCD:367US
; CURRENT APPLICATION NUMBER: US/10/077,584
; CURRENT FILING DATE: 2002-02-15

; PRIOR APPLICATION NUMBER: 60/369,157
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-077-584-8

Query Match 54.3%; Score 44; DB 14; Length 352;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
Db 59 QKREIYDQYG 68

RESULT 100

US-10-425-115-304214
; Sequence 304214, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 304214
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(363)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_40514C.1.pep
US-10-425-115-304214

Query Match 54.3%; Score 44; DB 16; Length 363;
Best Local Similarity 53.3%; Pred. No. 33;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 66 EKREIYDQYGEDAIK 80

Search completed: September 2, 2005, 21:08:50
Job time : 168 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 2, 2005, 20:48:00 ; Search time 16 Seconds
(without alignments)
90.203 Million cell updates/sec

Title: US-09-616-247-4

Perfect score: 81

Sequence: 1 QKRAAYDQYGHAAFE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	376	1	HHECDJ
2	81	100.0	376	2	G90630
3	81	100.0	376	2	G85481
4	81	100.0	379	2	AF0503
5	81	100.0	379	2	AB0058
6	81	100.0	394	2	C64112
7	78	96.3	381	2	D82270
8	77	95.1	392	2	S15295
9	75	92.6	377	2	F84947
10	75	92.6	377	2	JC5609
11	73	90.1	373	2	D81242
12	73	90.1	375	2	B47042
13	73	90.1	377	2	D97373
14	73	90.1	377	2	AD2591
15	73	90.1	377	2	AC3502
16	64	79.0	370	2	C71729
17	63	77.8	376	2	E70361
18	62	76.5	190	2	B33588
19	62	76.5	377	2	A83052
20	60	74.1	373	2	H97728
21	59	72.8	367	2	I40843
22	58	71.6	379	2	H86902
23	58	71.6	379	2	A47079
24	58	71.6	385	2	C87250
25	57	70.4	352	2	A49210
26	57	70.4	364	2	D70164
27	57	70.4	376	2	AD1621
28	57	70.4	377	2	T43739
29	57	70.4	377	2	AH1258

30	56	69.1	368	2	F82570	DnaJ protein Xf233
31	56	69.1	372	2	H97928	heat-shock protein
32	56	69.1	378	2	D95060	dnaJ protein [impo
33	53	65.4	499	2	G96831	hypothetical prote
34	52	64.2	372	2	B41874	heat shock protein
35	52	64.2	376	2	H69038	heat shock protein
36	52	64.2	389	2	S41748	heat shock protein
37	50	61.7	297	2	G81329	probable curved-DN
38	50	61.7	348	2	T04618	heat shock protein
39	50	61.7	379	2	B89939	DnaJ protein [impo
40	50	61.7	383	2	E90603	heat shock protein
41	50	61.7	416	2	F71379	heat shock protein
42	49	60.5	370	2	D83818	heat-shock protein
43	49	60.5	375	2	D82894	heat shock protein
44	49	60.5	498	2	T06594	heat shock protein
45	48	59.3	380	2	JC4739	heat shock protein
46	48	59.3	385	1	S29852	ADP,ATP carrier pr
47	48	59.3	910	1	S73361	dnaJ homolog prote
48	47	58.0	337	2	G84590	probable heat shoc
49	47	58.0	511	2	S38898	heat shock protein
50	45	55.6	335	2	T48161	heat shock protein
51	45	55.6	346	2	B84502	probable DnaJ prot
52	45	55.6	389	2	A64202	heat shock protein
53	44	54.3	352	2	A39660	heat shock protein
54	44	54.3	373	2	F81333	chaperone DnaJ Cj1
55	44	54.3	386	2	T09709	ADP,ATP carrier pr
56	44	54.3	389	2	T44957	heat shock protein
57	44	54.3	391	2	B84207	heat shock protein
58	44	54.3	397	2	S33312	dnaJ protein - lee
59	44	54.3	413	2	S35581	dnaJ protein homol
60	44	54.3	417	2	JQ2142	chaperone ANJ1 pro
61	44	54.3	419	2	T07371	dnaJ protein homol
62	44	54.3	419	2	T01643	DnaJ protein homol
63	44	54.3	420	2	S71199	DnaJ protein homol
64	44	54.3	420	2	T49127	DnaJ protein homol
65	43	53.1	170	2	T09601	DnaJ protein homol
66	43	53.1	242	2	JC7933	spermatogenic cell
67	43	53.1	345	2	T08563	dnaJ-related prote
68	43	53.1	369	2	B72327	dnaJ protein - The
69	43	53.1	396	2	T06102	heat shock protein
70	42	51.9	372	2	T48660	heat shock protein
71	42	51.9	390	2	S73459	heat shock protein
72	42	51.9	392	2	D81683	dnaJ protein TC061
73	42	51.9	392	2	H71526	probable heat shoc
74	42	51.9	423	2	T43929	DnaJ protein homol
75	42	51.9	518	2	S42091	Tid(56) protein -
76	41	50.6	223	2	T12472	hypothetical prote
77	41	50.6	253	2	A97106	response regulator
78	41	50.6	302	2	T39146	hypothetical prote
79	41	50.6	349	2	E86237	protein F14N23.23
80	41	50.6	369	2	G71831	co-chaperone with
81	41	50.6	369	2	D64686	co-chaperone and h
82	41	50.6	379	2	S21313	ADP,ATP carrier pr
83	41	50.6	379	2	S55900	DNAJ-like protein
84	41	50.6	379	2	T41633	psi protein - firs
85	41	50.6	391	2	G84611	probable DnaJ prot
86	41	50.6	418	2	S42031	LDJ2 protein - lee
87	41	50.6	423	2	T09338	DnaJ-like protein
88	41	50.6	528	2	T41362	hypothetical prote
89	41	50.6	559	2	JT0949	egg-specific prote
90	40	49.4	237	2	B82292	response regulator
91	40	49.4	241	2	B69655	two-component resp
92	40	49.4	313	2	S43888	3-isopropylmalate
93	40	49.4	356	2	E81130	3-isopropylmalate
94	40	49.4	356	2	E81836	probable 3-isoprop
95	40	49.4	385	2	D95350	probable transmemb
96	40	49.4	401	2	T18661	hypothetical prote
97	40	49.4	407	2	T39658	probable mitochond
98	40	49.4	420	2	F75396	dnaJ protein - Dei
99	40	49.4	601	1	A64222	heat shock protein
100	40	49.4	620	2	A83182	hypothetical prote

ALIGNMENTS

```
RESULT 1
HHECDJ
heat shock protein dnaJ - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: A92572; A26298; S40537; G64721; A26299
R:Bardwell, J.C.A.; Tilly, K.; Craig, E.; King, J.; Zyllicz, M.; Georgopoulos, C.
J. Biol. Chem. 261, 1782-1785, 1986
A:Title: The nucleotide sequence of the Escherichia coli K12 dnaJ gene.
A:Reference number: A92572; MUID:86111850; PMID:3003085
A:Accession: A92572
A:Molecule type: DNA
A:Residues: 1-376 <BAR>
A:Cross-references: UNIPROT:P08622; GB:M12565; NID:G145767; PIDN:AAA23693.1; PID:G145769
A:Experimental source: strain K12
R:Ohki, M.; Tamura, F.; Nishimura, S.; Uchida, H.
J. Biol. Chem. 261, 1778-1781, 1986
A:Title: Nucleotide sequence of the Escherichia coli dnaJ gene and purification of the g
A:Reference number: A26298; MUID:86111849; PMID:3003084
A:Accession: A26298
A:Molecule type: DNA
A:Residues: 1-376 <OHK>
A:Cross-references: GB:D10483; GB:J01597; GB:J01683; GB:J01706; GB:K01298; GB:K01990; GB
R:Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobu
submitted to the EMBL Data Library, December 1992
A:Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2
A:Reference number: S40531
A:Accession: S40537
A:Molecule type: DNA
A:Residues: 1-376 <YUR>
A:Cross-references: EMBL:D10483; NID:G216434; PIDN:BAA01292.1; PID:G216441
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shaoh, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G64721
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-376 <BLAT>
A:Cross-references: GB:AE000112; GB:U00096; NID:G1786192; PIDN:AACT3126.1; PID:G1786197;
A:Experimental source: strain K-12, substrain MG1655
C:Comment: This protein is induced by heat shock under the control of the htpR gene prod
C:Genetics:
A:Gene: dnaJ
A:Map position: 0 min
A:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein
F:5-70/Domain: dnaJ amino-terminal homology <DNJ>
F:77-106/Region: G/F motif
F:144-151/Region: CXXCXGXG repeat
F:161-168/Region: CXXCXGXG repeat
F:183-190/Region: CXXCXGXG repeat
F:197-204/Region: CXXCXGXG repeat

Query Match 100.0%; Score 81; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 2
G90630
DnaJ protein [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: G90630
```

```
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G90630
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <HAY>
A:Cross-references: UNIPROT:Q8XA65; UNIPROT:Q8FLC5; GB:BA000007; PIDN:BA833438.1; PID:G1
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC80015
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 81; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 3
G85481
Chaperone with DnaK, heat shock protein [imported] - Escherichia coli (strain O157:H7, s
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85481
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85481
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <STO>
A:Cross-references: UNIPROT:Q8XA65; UNIPROT:Q8FLC5; GB:AE005174; NID:G12512693; PIDN:AAG
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 81; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 4
AF0503
DnaJ protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF0503
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0503
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01166.1; PID:G16501296; GSPDB:GN00176
```


C:Genetics:

A:Gene: STY0013

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 81; DB 2; Length 379;

Best Local Similarity 100.0%; Pred. No. 1.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 61 QKRAAYDQYGHAAFE 75

RESULT 5

AB0058

Chaperone protein DnaJ [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: AB0058

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

ilo, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-379 <KUR>

A:Cross-references: UNIPROT:Q8ZIM6; GB:AL590842; PIDN:CAC99325.1; PID:gl5978561; GSPDB:G

C:Genetics:

A:Gene: dnaJ

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 81; DB 2; Length 379;

Best Local Similarity 100.0%; Pred. No. 1.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 61 QKRAAYDQYGHAAFE 75

RESULT 6

C64112

heat shock protein dnaJ - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 20-Aug-1999

C:Accession: C64112

R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: C64112

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-394 <TIGR>

A:Cross-references: GB:L42023; GB:U32803; NID:gl574162; PIDN:AAC22890.1; PID:gl574168; T

C:Genetics:

A:Gene: dnaJ

A:Start codon: GTG

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein

F;17-82/Domain: dnaJ amino-terminal homology <DNJ>

F;89-121/Region: G/F motif

F;159-166/Region: CXXCXGXG repeat

F;176-183/Region: CXXCXGXG repeat

F;198-205/Region: CXXCXGXG repeat

F;212-219/Region: CXXCXGXG repeat

Query Match 100.0%; Score 81; DB 2; Length 394;

Best Local Similarity 100.0%; Pred. No. 1.5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 73 QKRAAYDQYGHAAFE 87

RESULT 7

D82270

dnaJ protein VC0856 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: D82270

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.

chardson, D.; Esmailieva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers,

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: D82270

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-381 <HEI>

A:Cross-references: UNIPROT:O34242; GB:AE004171; GB:AE003852; NID:g9655308; PIDN:AAF940

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0856

A:Map position: 1

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 96.3%; Score 78; DB 2; Length 381;

Best Local Similarity 93.3%; Pred. No. 4.9e-06;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 61 QKRAAYDQYGHAAFE 75

RESULT 8

S15295

nolC protein - Rhizobium fredii

C:Species: Rhizobium fredii

C:Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: S15295

R:Krishnan, H.B.; Pueppke, S.G.

Mol. Microbiol. 5, 737-745, 1991

A:Title: nolC, a Rhizobium fredii gene involved in cultivar-specific nodulation of soyb

A:Reference number: S15295; MUID:91260457; PMID:1646377

A:Accession: S15295

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-392 <MOL>

A:Cross-references: UNIPROT:P26508; GB:I03521; NID:gl52353; PIDN:AAA26333.1; PID:gl5235

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

F;4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 95.1%; Score 77; DB 2; Length 392;

Best Local Similarity 93.3%; Pred. No. 7.6e-06;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 60 QKRAAYDQYGHAAFE 74

RESULT 9

P84947

dnaJ protein [imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C;Accession: F84947
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: F84947
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: dnaJ; BU152
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 92.6%; Score 75; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. No. 1.7e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 61 EKRSAYDQYGHAAFE 75

RESULT 10

JC5609
heat shock protein dnaJ - Buchnera sp.
C;Species: Buchnera sp.
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C;Accession: JC5609
R;Sato, S.; Ishikawa, H.
J. Biochem. 122, 41-48, 1997
A;Title: Structure and expression of the dnaKJ operon of Buchnera, an intracellular symbiont of aphids
A;Reference number: JC5608; MUID:97420684; PMID:9276669
A;Accession: JC5609
A;Molecule type: DNA
A;Residues: 1-377 <SAT>
A;Cross-references: DDBJ:D88673; NID:g2351215; PIDN:BAA21965.1; PID:g2351217
C;Comment: This protein binds to DnaK protein and GrpE protein and modulates the chaperone activity
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone
F:5-70/Domain: dnaJ amino-terminal homology <DNJ>
F:77-108/Region: G/F motif
F:145-152/Region: CXXCXGKG repeat
F:162-169/Region: CXXCXGKG repeat
F:184-191/Region: CXXCXGKG repeat
F:198-205/Region: CXXCXGKG repeat

Query Match 92.6%; Score 75; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. No. 1.7e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 61 EKRSAYDQYGHAAFE 75

RESULT 11

DB1242
DnaJ protein NMA0209 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain 29972)
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: DB1242; C82015
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: AB1000; MUID:20175755; PMID:10710307
A;Accession: DB1242

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A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-373 <TET>
A:Cross-references: UNIPROT:p57107; GB:AE002366; GB:AE002098; NID:g7225284; PIDN:AAF4052
A:Experimental source: serogroup B, strain MCS8
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
i; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: AB1775; MUID:20222556; PMID:10761919
A:Accession: C92015
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-373 <PAR>
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83522.1; PID:g737897
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: dnaJ; NMB0059; NMA0209
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 373;
Best Local Similarity 86.7%; Pred. No. 3.7e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
:|||||:|||||
Db 61 EKRAAYDQYGHAAFE 75

RESULT 12
B47042
heat shock protein dnaJ - Brucella ovis
C:Species: Brucella ovis
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B47042
R:Cellier, M.F.; Teyssier, J.; Nicolas, M.; Liautard, J.P.; Marti, J.; Sri Widada, J.
J. Bacteriol. 174, 8036-8042, 1992
A:Title: Cloning and characterization of the Brucella ovis heat shock protein DnaK func
A:Reference number: A47042; MUID:93094135; PMID:1459952
A:Accession: B47042
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-375 <CE>
A:Cross-references: UNIPROT:Q05980; EMBL:M95799; NID:g144114; PIDN:AAC36133.1; PID:g1441
A:Note: sequence extracted from NCBI backbone (NCBI:119966, NCBIP:119968)
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: DNA replication; heat shock; molecular chaperone
F:4-69/Domain: dnaJ amino-terminal homology <DNJ>
F:76-108/Region: G/F motif
F:146-153/Region: CXXCXGXG repeat
F:163-170/Region: CXXCXGXG repeat
F:185-192/Region: CXXCXGXG repeat
F:199-206/Region: CXXCXGXG repeat

Query Match 90.1%; Score 73; DB 2; Length 375;
Best Local Similarity 86.7%; Pred. No. 3.7e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
:|||||:|||||
Db 60 QKRAAYDRFGHAAFE 74

RESULT 13
D97373
chaperone protein dnaJ [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: D97373
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, D.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.

```

Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* strain C58
 A/Reference number: A97359; MUID:21608551; PMID:11743194
 A/Accession: D97373
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-377 <KUR>
 A/Cross-references: UNIPROT:P50018; GB:AE007869; PIDN:AAK85941.1; PID:g15154994; GSPDB:C58
 C/Genetics:
 A:Gene: AGR_C192
 A:Map position: circular chromosome
 C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 377;
 Best Local Similarity 86.7%; Pred. No. 3.7e-05;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
 Db 61 QKRAAYDRFGHAAFE 75

RESULT 14
 AD2591
 molecular chaperone, DnaJ family dnaJ [imported] - *Agrobacterium tumefaciens* (strain C58)
 C/Species: *Agrobacterium tumefaciens*
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C/Accession: AD2591
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
 A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A/Reference number: AB2577; MUID:21608550; PMID:11743193
 A/Accession: AD2591
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-377 <KUR>
 A/Cross-references: UNIPROT:P50018; GB:AE008688; PIDN:AAJ41146.1; PID:g17738442; GSPDB:C58
 A/Experimental source: strain C58 (Dupont)
 C/Genetics:
 A:Gene: dnaJ
 A:Map position: circular chromosome
 C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 377;
 Best Local Similarity 86.7%; Pred. No. 3.7e-05;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
 Db 61 QKRAAYDRFGHAAFE 75

RESULT 15
 AC3502
 chaperone protein dnaJ [imported] - *Brucella melitensis* (strain 16M)
 C/Species: *Brucella melitensis*
 C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C/Accession: AC3502
 R/DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Los, T.; Ivanova, I.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A>Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A/Reference number: AD3252; PMID:11756688
 A/Accession: AC3502
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-377 <KUR>
 A/Cross-references: UNIPROT:Q8VE77; UNIPROT:Q8FXX1; GB:AE008917; PIDN:AAJ53182.1; PID:g15154994
 A/Experimental source: strain 16M

C/Genetics:

A:Gene: BMEI2001

A:Map position: I

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match

90.1%; Score 73; DB 2; Length 377;

Best Local Similarity 86.7%; Pred. No. 3.7e-05;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 60 QKRAAYDRFGHAAFE 74

RESULT 16

C71729

dnaJ protein (dnaJ) RP184 - *Rickettsia prowazekii*C/Species: *Rickettsia prowazekii*

C/Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C/Accession: C71729

R/Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Alsmark, Nature 396, 133-140, 1998

A>Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.

A/Reference number: A71630; MUID:99039499; PMID:9823893

A/Accession: C71729

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-370 <AND>

A/Cross-references: UNIPROT:Q9ZDV0; GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA146

A/Experimental source: strain Madrid E

C/Genetics:

A:Gene: dnaJ; RP184

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

P/4-68/Domain: dnaJ amino-terminal homology <DNJ>

Query Match

79.0%; Score 64; DB 2; Length 370;

Best Local Similarity 73.3%; Pred. No. 0.0014;

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 59 QKRAAYDRFGHDAFQ 73

RESULT 17

E70361

chaperone DnaJ - *Aquifex aeolicus*C/Species: *Aquifex aeolicus*

C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C/Accession: E70361

R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V. Nature 392, 353-358, 1998

A>Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.

A/Reference number: A70300; MUID:98196666; PMID:9537320

A/Accession: E70361

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-376 <AQF>

A/Cross-references: UNIPROT:O66921; GB:AE000703; NID:g2983287; PIDN:AAO6881.1; PID:g29

A/Experimental source: strain VF5

C/Genetics:

A:Gene: dnaJ2

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

P/8-72/Domain: dnaJ amino-terminal homology <DNJ>

Query Match

77.8%; Score 63; DB 2; Length 376;

Best Local Similarity 73.3%; Pred. No. 0.0022;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 63 EKRLYDMYGHAAFE 77

```
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: H97728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <KUR>
A;Cross-references: UNIPROT:Q92J37; GB:AE006914; PIDN:AAI02770.1; PID:gl5619285; GSPDB:G
C;Genetics:
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 74.1%; Score 60; DB 2; Length 373;
Best Local Similarity 73.3%; Pred. No. 0.0074;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 59 QKRAAYDELGHDAFQ 73

RESULT 21
I40843
heat shock protein dnaJ - Coxiella burnetii
C;Species: Coxiella burnetii
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40843
R;Zuber, M.; Hoover, T.A.; Court, D.L.
Gene 152, 99-102, 1995
A;Title: Cloning, sequencing and expression of the dnaJ gene of Coxiella burnetii.
A;Reference number: I40843; MUID:95129924; PMID:7828937
A;Accession: I40843
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-367 <RES>
A;Cross-references: UNIPROT:P42381; GB:L36455; NID:g547392; PIDN:AAA65100.1; PID:G547399
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone
F;5-70/Domain: dnaJ amino-terminal homology <DNJ>
F;77-108/Region: G/F motif
F;146-153/Region: CXXCXGXG repeat
F;162-169/Region: CXXCXGXG repeat
F;184-191/Region: CXXCXGXG repeat
F;198-205/Region: CXXCXGXG repeat

Query Match 72.8%; Score 59; DB 2; Length 367;
Best Local Similarity 66.7%; Pred. No. 0.011;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 KKRASYDQFGHAGVE 75

RESULT 22
H86902
DnaJ protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86902
R;Polotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Cross-references: UNIPROT:P35514; GB:AE005176; PID:g12725291; PIDN:AAK06322.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
```

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Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: H97728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <KUR>
A;Cross-references: UNIPROT:Q92J37; GB:AE006914; PIDN:AAI02770.1; PID:gl5619285; GSPDB:G
C;Genetics:
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 74.1%; Score 60; DB 2; Length 373;
Best Local Similarity 73.3%; Pred. No. 0.0074;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 59 QKRAAYDELGHDAFQ 73

RESULT 21
I40843
heat shock protein dnaJ - Coxiella burnetii
C;Species: Coxiella burnetii
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40843
R;Zuber, M.; Hoover, T.A.; Court, D.L.
Gene 152, 99-102, 1995
A;Title: Cloning, sequencing and expression of the dnaJ gene of Coxiella burnetii.
A;Reference number: I40843; MUID:95129924; PMID:7828937
A;Accession: I40843
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-367 <RES>
A;Cross-references: UNIPROT:P42381; GB:L36455; NID:g547392; PIDN:AAA65100.1; PID:G547399
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone
F;5-70/Domain: dnaJ amino-terminal homology <DNJ>
F;77-108/Region: G/F motif
F;146-153/Region: CXXCXGXG repeat
F;162-169/Region: CXXCXGXG repeat
F;184-191/Region: CXXCXGXG repeat
F;198-205/Region: CXXCXGXG repeat

Query Match 72.8%; Score 59; DB 2; Length 367;
Best Local Similarity 66.7%; Pred. No. 0.011;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 KKRASYDQFGHAGVE 75

RESULT 22
H86902
DnaJ protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86902
R;Polotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Cross-references: UNIPROT:P35514; GB:AE005176; PID:g12725291; PIDN:AAK06322.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
```

```
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: H97728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <KUR>
A;Cross-references: UNIPROT:Q92J37; GB:AE006914; PIDN:AAI02770.1; PID:gl5619285; GSPDB:G
C;Genetics:
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 74.1%; Score 60; DB 2; Length 373;
Best Local Similarity 73.3%; Pred. No. 0.0074;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 59 QKRAAYDELGHDAFQ 73

RESULT 21
I40843
heat shock protein dnaJ - Coxiella burnetii
C;Species: Coxiella burnetii
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40843
R;Zuber, M.; Hoover, T.A.; Court, D.L.
Gene 152, 99-102, 1995
A;Title: Cloning, sequencing and expression of the dnaJ gene of Coxiella burnetii.
A;Reference number: I40843; MUID:95129924; PMID:7828937
A;Accession: I40843
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-367 <RES>
A;Cross-references: UNIPROT:P42381; GB:L36455; NID:g547392; PIDN:AAA65100.1; PID:G547399
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone
F;5-70/Domain: dnaJ amino-terminal homology <DNJ>
F;77-108/Region: G/F motif
F;146-153/Region: CXXCXGXG repeat
F;162-169/Region: CXXCXGXG repeat
F;184-191/Region: CXXCXGXG repeat
F;198-205/Region: CXXCXGXG repeat

Query Match 72.8%; Score 59; DB 2; Length 367;
Best Local Similarity 66.7%; Pred. No. 0.011;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 KKRASYDQFGHAGVE 75

RESULT 22
H86902
DnaJ protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86902
R;Polotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Cross-references: UNIPROT:P35514; GB:AE005176; PID:g12725291; PIDN:AAK06322.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
```

A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 71.6%; Score 58; DB 2; Length 379;
Best Local Similarity 91.7%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
Db 60 QKRAAYDQYGEA 71

RESULT 23

A47079
heat shock protein dnaJ - Lactococcus lactis
C:Species: Lactococcus lactis
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47079
R:van Aseeldonk, M.; Simons, A.; Visser, H.; de Vos, W.M.; Simons, G.
J. Bacteriol. 175, 1637-1644, 1993
A:Title: Cloning, nucleotide sequence, and regulatory analysis of the Lactococcus lactis
A:Reference number: A47079; MUID:93194788; PMID:8449872
A:Contents: NIZO R5
A:Accession: A47079
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-379 <VAN>
A:Cross-references: UNIPROT:P35514; EMBL:M99413; NID:G293012
A:Experimental source: strain NIZO R5
A:Note: sequence extracted from NCBI backbone (NCBIN:127395, NCBIP:127396)
C:Genetics:

A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: DNA replication; heat shock; molecular chaperone
F:5-69/Domain: dnaJ amino-terminal homology <DNJ>
F:76-114/Region: G/F motif
F:154-161/Region: CXXCXGXG repeat
F:171-178/Region: CXXCXGXG repeat
F:197-204/Region: CXXCXGXG repeat
F:211-218/Region: CXXCXGXG repeat

Query Match 71.6%; Score 58; DB 2; Length 379;
Best Local Similarity 91.7%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
Db 60 QKRAAYDQYGEA 71

RESULT 24

C87250
dnaJ protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87250
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87250
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-385 <STO>
A:Cross-references: UNIPROT:P22305; GB:AE005673; NID:G13421099; PIDN:AAK21999.1; GSPDB:G
C:Genetics:

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 71.6%; Score 58; DB 2; Length 385;
Best Local Similarity 83.3%; Pred. No. 0.017;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
Db 59 QKRAAYDRFGHA 70

RESULT 25

A49210
heat shock protein dnaJ - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Aug-1998
C:Accession: A49210
R:Anzola, J.; Luft, B.J.; Gorgone, G.; Peltz, G.
Infect. Immun. 60, 4965-4968, 1992
A:Title: Characterization of a Borrelia burgdorferi dnaJ homolog.
A:Reference number: A49210; MUID:93014224; PMID:1193161
A:Accession: A49210
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-352 <ANZ>
A:Note: sequence extracted from NCBI backbone (NCBIN:116537, NCBIP:116539)
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F:4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 70.4%; Score 57; DB 2; Length 352;
Best Local Similarity 64.3%; Pred. No. 0.024;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAF 15
Db 61 KKAKYDRFGHSAF 74

RESULT 26

D70164
heat shock protein dnaJ-1 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: D70164; S30946
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: D70164
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-364 <KLE>
A:Cross-references: UNIPROT:P28616; GB:AE001154; GB:AE000783; NID:G2688431; PIDN:AAC668

A:Experimental source: strain B31
R:Fillly, K.; Hauser, R.; Campbell, J.; Oestheimer, G.J.
Mol. Microbiol. 7, 359-369, 1993
A:Title: Isolation of dnaJ, dnaK, and grpE homologues from Borrelia burgdorferi and cor
A:Reference number: S30944; MUID:93211279; PMID:8459764
A:Accession: S30946
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <TIL>
A:Cross-references: EMBL:M96847
C:Genetics:

A:Start codon: GTG
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F:4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 70.4%; Score 57; DB 2; Length 364;
Best Local Similarity 64.3%; Pred. No. 0.025;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAF 15
Db 61 KKAKYDRFGHSAF 74

```
Db 61 KKAKYDRFGHSAFE 74

RESULT 27
AD1621
heat shock protein DnaJ [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD1621
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1621
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <GLA>
A:Cross-references: UNIPROT:Q9S5A3; GB:NC_003210; PIDN:CAC99550.1; PID:g16410901; GSPDB:G
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 70.4%; Score 57; DB 2; Length 377;
Best Local Similarity 90.9%; Pred. No. 0.026;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11
|||||
Db 60 QKRAQYDQYGH 70

RESULT 30
F82570
DnaJ protein XP2339 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: F82570
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: F82570
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <STM>
A:Cross-references: UNIPROT:Q9PB06; GB:AE004044; GB:AE003849; NID:g9107501; PIDN:AAF8513
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrex, H.
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XP2339
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 69.1%; Score 56; DB 2; Length 368;
Best Local Similarity 66.7%; Pred. No. 0.037;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
:|||||
Db 61 KKRKLYDTHGHAAFE 75

RESULT 31
H97928
```

heat-shock protein (activation of DnaK) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: H97928
R:Hookins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: H97928
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-372 <KUR>
A:Cross-references: UNIPROT:Q8CWT2; GB:AE007317; PIDN:AAK99260.1; PID:gl5458025; GSPDB:G
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 69.1%; Score 56; DB 2; Length 372;
Best Local Similarity 91.7%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
| | | | | | | | | | | | | | | |
Db 60 QKRAAYDQYGA 71

RESULT 32
D95060
dnaJ protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: D95060
R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: D95060
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <KUR>
A:Cross-references: UNIPROT:P95830; GB:AE005672; PIDN:AAK74677.1; PID:gl4971993; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0519
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 69.1%; Score 56; DB 2; Length 378;
Best Local Similarity 91.7%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
| | | | | | | | | | | | | | | |
Db 60 QKRAAYDQYGA 71

RESULT 33
G96831
hypothetical protein F18B13.12 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: G96831
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G96831
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-499 <STO>
A:Cross-references: UNIPROT:Q9SSD4; GB:AE005173; NID:gs902381; PIDN:AAD55483.1; GSPDB:B
C:Genetics:
A:Gene: F18B13.12
A:Map position: 1
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 65.4%; Score 53; DB 2; Length 499;
Best Local Similarity 83.3%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
| | | | | | | | | | | | | | | |
Db 130 QKRAAYDQYGE 141

RESULT 34
B41874
heat shock protein dnaJ - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 03-May-1994 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: B41874; S09501; G69617; S27506
R:Wetstein, M.; Voelker, U.; Dedio, J.; Loebau, S.; Zuber, U.; Schieswohl, M.; Herget
J. Bacteriol. 174, 3300-3310, 1992
A:Title: Cloning, sequencing, and molecular analysis of the dnaK locus from Bacillus su
A:Reference number: A41874; MUID:92250426; PMID:1339421
A:Accession: B41874
A:Molecule type: DNA
A:Residues: 1-372 <WET>
A:Cross-references: UNIPROT:PI7631; EMBL:M84964; NID:gl43056; PIDN:AAA22529.1; PID:gl43
R:Wetstein, M.; Dedio, J.; Schumann, W.
Nucleic Acids Res. 18, 2172, 1990
A:Title: Complete nucleotide sequence of the Bacillus subtilis dnaK gene.
A:Reference number: S09500; MUID:90245667; PMID:2110662
A:Accession: S09501
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-24 <WET>
A:Cross-references: EMBL:X52064; NID:G93888; PIDN:CAA36287.1; PID:gs9890
R:Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maseuda, S.; Maue
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, F.; Tognoni, J.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: G69617
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-372 <KUN>
A:Cross-references: GB:Z99117; GB:AL009126; NID:gs2634966; PIDN:CAB14488.1; PID:gs2634992
A:Experimental source: strain 168
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein

F:5-69/Domain: dnaJ amino-terminal homology <DNJ>

F:76-105/Region: G/F motif
F:145-152/Region: CXXCXGXG repeat
F:162-169/Region: CXXCXGXG repeat
F:188-195/Region: CXXCXGXG repeat
F:202-209/Region: CXXCXGXG repeat

Query Match 64.2%; Score 52; DB 2; Length 372;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11
:|||||:|
Db 60 QKRAHYDQFGH 70

RESULT 35

H69038 heat shock protein dnaJ - Methanobacterium thermoautotrophicum (strain Delta H)

C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: H69038
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func0
A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: H69038

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-376 <MTH>

A:Cross-references: UNIPROT:O27352; GB:AE000894; GB:AE000666; NID:g2622392; PIDN:AAB8577

A:Experimental source: strain Delta H

C:Genetic:

A:Gene: MTH1291

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: DNA replication; heat shock; molecular chaperone

F:5-69/Domain: dnaJ amino-terminal homology <DNJ>

F:75-111/Region: G/F motif

F:148-155/Region: CXXCXGXG repeat

F:165-172/Region: CXXCXGXG repeat

F:191-198/Region: CXXCXGXG repeat

F:205-212/Region: CXXCXGXG repeat

Query Match 64.2%; Score 52; DB 2; Length 376;
Best Local Similarity 53.3%; Pred. No. 0.2;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
:|||||:|
Db 60 EKRAHYDQFGHMD 74

RESULT 36

S41748

heat shock protein dnaJ - Methanosarcina mazei

C:Species: Methanosarcina mazei

C:Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C:Accession: S41748; S41150

R:Conway de Macario, E.

submitted to the EMBL Data Library, April 1992

A:Reference number: S41748

A:Accession: S41748

A:Molecule type: DNA

A:Residues: 1-389 <CON>

A:Cross-references: UNIPROT:P35515; EMBL:X60265; NID:g48938; PIDN:CAA42813.1; PID:g48940

A:Experimental source: strain S-6

R:Macario, A.J.L.; Dugan, C.B.; Clarens, M.; Conway de Macario, E.

Nucleic Acids Res. 21, 2773, 1993

A:Title: dnaJ in Archaea.

A:Reference number: S41150; MUID:93324351; PMID:8332479

A:Accession: S41150

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 4-208 <MAC>

A:Cross-references: EMBL:X60265; NID:g48938; PIDN:CAA42813.1; PID:g48940

A:Experimental source: strain S-6

C:Genetic:

A:Gene: dnaJ

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein

F:6-70/Domain: dnaJ amino-terminal homology <DNJ>

F:77-104/Region: G/F motif

F:144-151/Region: CXXCXGXG repeat

F:161-168/Region: CXXCXGXG repeat

F:187-194/Region: CXXCXGXG repeat

F:201-208/Region: CXXCXGXG repeat

Query Match 64.2%; Score 52; DB 2; Length 389;
Best Local Similarity 53.3%; Pred. No. 0.2;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
:|||||:|
Db 61 EKRAQYDRFGHAGID 75

RESULT 37

GB1329

probable curved-DNA binding protein Cj1229 [imported] - Campylobacter jejuni (strain NCTC

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: GB1329

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Bagham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: AB1250; MUID:20150912; PMID:10688204

A:Accession: GB1329

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-297 <PAR>

A:Cross-references: UNIPROT:Q9PN68; GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB7348

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetic:

A:Gene: cbpA; Cj1229

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 61.7%; Score 50; DB 2; Length 297;
Best Local Similarity 64.3%; Pred. No. 0.35;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAAF 14
:|||||:|
Db 58 KKRAQYDQYGDMSMF 71

RESULT 38

T04618

heat shock protein homolog F2009.160 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T04618

R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, October 1998

A:Reference number: Z15380

A:Accession: T04618

A:Molecule type: DNA

A:Residues: 1-348 <BEV>

A:Cross-references: UNIPROT:O49457; EMBL:AL021749

A:Experimental source: cultivar Columbia; BAC clone F2009

C:Genetic:

A:Map position: 4

A:Introns: 55/3; 204/2

A>Note: F2009.160

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F:4-70/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 61.7%; Score 50; DB 2; Length 348;
Best Local Similarity 90.0%; Pred. No. 0.41; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
|||||
Db 61 QKRAVDQYG 70

RESULT 39

B89939
DnaJ protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89939
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89939
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <KUR>
A:Cross-references: UNIPROT:Q99TR8; GB:BA000018; PID:gl3701377; PIDN:BAB42671.1; GSPDB:Q
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 61.7%; Score 50; DB 2; Length 379;
Best Local Similarity 80.0%; Pred. No. 0.45;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGH 11
|||||
Db 61 KRAVDQFGH 70

RESULT 40

E90603
heat shock protein DnaJ (activation of DNak) [imported] - Mycoplasma pulmonis (strain UA
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: E90603
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallieson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: E90603
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <KUR>
A:Cross-references: UNIPROT:Q98PI9; GB:AL445566; PID:gl4090148; PIDN:CAC13906.1; GSPDB:Q
C:Genetics:
A:Gene: MYPU_7330
A:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 61.7%; Score 50; DB 2; Length 383;
Best Local Similarity 61.5%; Pred. No. 0.45;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAA 13
:|:|:|:|:|
Db 67 EKRAVDKYGHEA 79

RESULT 41

F71379
heat shock protein dnaJ - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 28-Aug-1998 #sequence_revision 28-Aug-1998 #text_change 17-Mar-1999
C:Accession: F71379
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McC
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: F71379
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-416 <COL>
A:Cross-references: GB:AE001203; GB:AE000520; NID:g33222476
A:Experimental source: strain Nichols
A:Note: This ORF is annotated but not translated in GenBank entry AE001203, release 107
C:Comment: This is the hypothetical translation of a sequence that was reported as a co
C:Comment: This translation was produced by PIR staff from information in the GenBank a
ion codon. A BLAST search of the GenBank database shows that, in the majority of cases,
C:Genetics:
A:Gene: TP0217

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein; t
F:48-113/Domain: dnaJ amino-terminal homology <DNJ>
F:325-326/Region: plus-two translational frameshift
Query Match 61.7%; Score 50; DB 2; Length 416;
Best Local Similarity 90.0%; Pred. No. 0.49;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
|||||
Db 104 QKRAAYDRYG 113

RESULT 42

D83818
heat-shock protein (activation of DnaK) dnaJ [imported] - Bacillus halodurans (strain C
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: D83818
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: D83818
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <STO>
A:Cross-references: UNIPROT:Q9KD71; GB:AP001511; GB:BA000004; NID:gl0173727; PIDN:BA005
A:Experimental source: strain C-125
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 60.5%; Score 49; DB 2; Length 370;
Best Local Similarity 72.7%; Pred. No. 0.65;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 11
||:|:|:|:|
Db 60 QKRAHYDQFGH 70

RESULT 43

D82894
heat shock protein UU407 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: D82894

R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseil, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: D82894
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-375 <GLA>
A:Cross-references: GB:AE002138; GB:AF222894; NID:g6899390; PIDN:AAF30818.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: dnaJ; U0407
A:Genetic code: SGC3
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 60.5%; Score 49; DB 2; Length 375;
Best Local Similarity 72.7%; Pred. No. 0.66;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11
:|||||:
Db 59 KKRQYDQFGH 69

RESULT 44
T06594
heat shock protein dnaJ - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06594
R:Schlacher, T.; Soll, J.
submitted to the EMBL Data Library, July 1997
A:Description: DnaJ and GrpE homologues in pea chloroplasts.
A:Reference number: Z15784
A:Accession: T06594
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-498 <SCH>
A:Cross-references: UNIPROT:P92424; EMBL:Z71640; PIDN:CAA96305.1
A:Experimental source: var. Golf
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: chloroplast; heat shock; stress-induced protein
F:71-135/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 60.5%; Score 49; DB 2; Length 498;
Best Local Similarity 75.0%; Pred. No. 0.89;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
:|||||:
Db 126 KKRALYDQYGEA 137

RESULT 45
JC4739
heat shock protein dnaJ - Bacillus stearothermophilus
C:Species: Bacillus stearothermophilus
C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4739
R:Herbert, M.; Schoen, U.; Angermann, K.; Lang, J.; Schumann, W.
Gene 170, 81-84, 1996
A:Title: Cloning and sequencing of the dnaK operon of Bacillus stearothermophilus.
A:Reference number: JC4738; MUID:96200860; PMID:8621094
A:Accession: JC4739
A:Molecule type: DNA
A:Residues: 1-380 <HER>
A:Cross-references: UNIPROT:Q45552; EMBL:X90709; NID:g1568471; PIDN:CAA62240.1; PID:g156
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein

F:5-69/Domain: dnaJ amino-terminal homology <DNJ>
F:76-108/Region: G/F motif
F:148-155/Region: CXXCXGXG repeat
F:165-172/Region: CXXCXGXG repeat
F:191-198/Region: CXXCXGXG repeat
F:205-212/Region: CXXCXGXG repeat

Query Match 59.3%; Score 48; DB 2; Length 380;
Best Local Similarity 75.0%; Pred. No. 1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
:|||||:
Db 60 QKRAHYDQFGQA 71

RESULT 46
S29852
ADP,ATP carrier protein - Arabidopsis thaliana
N:Alternate names: adenine nucleotide translocator
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S29852; S29618
R:Schuster, W.; Kloos, S.; Brennicke, A.
Biochim. Biophys. Acta 1172, 205-208, 1993
A:Title: An adenine nucleotide translocator gene from Arabidopsis thaliana.
A:Reference number: S29852; MUID:93176813; PMID:8439563
A:Accession: S29852
A:Molecule type: DNA
A:Residues: 1-385 <SCH>
A:Cross-references: UNIPROT:P40941; EMBL:X68592; NID:g16159; PIDN:CAA48579.1; PID:g16160
C:Genetics:
A:Gene: ANT2
A:Introns: 162/3; 287/3
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; mitochondrion; transmembrane protein
F:81-176/Domain: ADP,ATP carrier protein repeat homology <ACPL>
F:186-281/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:287-375/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 59.3%; Score 48; DB 1; Length 385;
Best Local Similarity 60.0%; Pred. No. 1;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAE 15
:|||||:
Db 41 QKHAAYGNYSNAFQ 55

RESULT 47
S73361
dnaJ homolog protein C09_orf910 - Mycoplasma pneumoniae (strain ATCC 29342)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: S73361
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73361
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-910 <HIM>
A:Cross-references: UNIPROT:P75354; EMBL:AE000004; GB:U00089; NID:g1673671; PIDN:AAB9568
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3
A:Superfamily: Mycoplasma heat shock protein dnaJ homolog C09_orf910; dnaJ amino-terminal
F:7-71/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 59.3%; Score 48; DB 1; Length 910;
Best Local Similarity 72.7%; Pred. No. 2.5;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGH 11
:|||||

Db 62 KKRANYDKYGH 72

RESULT 48
G84590
probable heat shock protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84590
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84590
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <STO>
A:Cross-references: UNIPROT:Q9SIL3; GB:A8002093; NID:94586038; PIDN:AAD25656.1; GSPDB:GN
C:Genetics:
A:Gene: At2g20560
A:Map position: 2
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 58.0%; Score 47; DB 2; Length 337;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGH 10
:|||||

Db 61 OKRAAYDOYGH 70

RESULT 49
S38898
heat shock protein MDJ1 precursor - yeast (Saccharomyces cerevisiae)
N:Alternate names: MDJ1 protein; protein YFL016C
C:Species: Saccharomyces cerevisiae
C:Date: 31-Dec-1993 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S38898; A48320; A53500; S56238; S62297
R;Rowley, N.K.; Prip-Buus, C.; Westermann, B.; Brown, C.M.; Schwarz, E.; Barrell, B.G.;
submitted to the EMBL Data Library, November 1993
A:Description: Mdj1p, a novel DnaJ homologue of Saccharomyces cerevisiae, plays a role in
A:Reference number: S38898
A:Accession: S38898
A:Molecule type: DNA
A:Residues: 1-511 <ROM>
A:Cross-references: UNIPROT:P35191; EMBL:Z28336; NID:9431909; PIDN:CAA82189.1; PID:94319
R;Churcher, C.
submitted to the EMBL Data Library, September 1994
A:Reference number: S48310
A:Accession: S48320
A:Molecule type: DNA
A:Residues: 1-511 <CHU>
A:Cross-references: EMBL:Z46255; NID:9559925; PIDN:CAA86351.1; PID:G559936; MIPS:YFL016C
R;Rowley, N.; Prip-Buus, C.; Westermann, B.; Brown, C.; Schwarz, E.; Barrell, B.; Neuph
Cell 77, 249-259, 1994
A:Title: Mdj1p, a novel chaperone of the DnaJ family, is involved in mitochondrial bioge
A:Reference number: A53500; MUID:94221642; PMID:8168133
A:Accession: A53500
A:Molecule type: DNA
A:Residues: 1-511 <RO2>
A:Cross-references: GB:Z28336; NID:9431909; PIDN:CAA82189.1; PID:9431910
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasam
submitted to the EMBL Data Library, May 1995
A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces ce
A:Reference number: S56186
A:Accession: S56238

A:Molecule type: DNA
A:Residues: 1-511 <MUR>
A:Cross-references: EMBL:D50617; NID:9836685; PIDN:BAA09222.1; PID:9836738; MIPS:YFL016C
R;Murakami, Y.
submitted to the EMBL Data Library, December 1994
A:Reference number: S62230
A:Accession: S62297
A:Molecule type: DNA
A:Residues: 1-511 <MUW>
A:Cross-references: EMBL:D44596; NID:g1100783; PIDN:BAA08001.1; PID:g1100788
C:Genetics:
A:Gene: SGD:MDJ1
A:Cross-references: SGD:S0001878; MIPS:YFL016C
A:Map position: 6L
A:Genome: nuclear
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: heat shock; membrane protein; mitochondrial inner membrane; mitochondrion;
F;1-55/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;56-511/Product: heat shock protein MDJ1 #status predicted <MAT>
F;61-125/Domain: dnaJ amino-terminal homology <DNU>

Query Match 58.0%; Score 47; DB 2; Length 511;
Best Local Similarity 69.2%; Pred. No. 2.1;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KRAAYDOYGHAAF 14
:|||||

Db 117 KROQYDQFGPAAP 129

RESULT 50
T48161
heat shock protein 40-like - Arabidopsis thaliana
N:Alternate names: protein T1008.100
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48161
R;Bevan, M.; Pohl, T.; Weizensegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24486
A:Accession: T48161
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <BEV>
A:Cross-references: UNIPROT:Q5M034; EMBL:AL161746
A:Experimental source: cultivar Columbia; BAC clone T1008
C:Genetics:
A:Map position: 5
A:Introns: 55/3; 190/2
A:Note: T1008.100
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;4-70/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 55.6%; Score 45; DB 2; Length 335;
Best Local Similarity 80.0%; Pred. No. 3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGH 10
:|||||

Db 61 OKRAAYEQYGH 70

RESULT 51
B84602
probable DnaJ protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84602
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Title: Characterization of SIS1, a Saccharomyces cerevisiae homologue of bacterial dna
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84602
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <STO>
A;Cross-references: UNIPROT:Q9SJS8; GB:AE002093; NID:g4567282; PIDN:AAD23695.1; GSPDB:GN
C;Genetics:
A;Gene: At2g21510
A;Map position: 2

Query Match 55.6%; Score 45; DB 2; Length 346;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYG 10
Db 63 KRAAYDKYG 71

RESULT 52
A64202
heat shock protein dnaJ - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: A64202; T09677
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:196026346; PMID:7569993
A;Accession: A64202
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-389 <TIGR>
A;Cross-references: UNIPROT:P47265; GB:U39680; GB:L43967; NID:g1045681; PID:g1045688; TI
A;Experimental source: strain G-37
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.L.; Nguyen, D.T.; Utterback, T.; Saudek, D.M.; Phillips, C.A.; Merrick
submitted to the EMBL Data Library, October 1998
A;Reference number: Z16818
A;Accession: T09677
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-389 <FRA>
A;Cross-references: EMBL:U39681; NID:g3844626; PID:g3844628
A;Experimental source: isolate G37
C;Genetics:
A;Gene: MG019
A;Genetic code: SGC3
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: molecular chaperone
F;7-77/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 55.6%; Score 45; DB 2; Length 389;
Best Local Similarity 63.6%; Pred. No. 3.5;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGH 11
Db 68 EKRRKYDQFGH 78

RESULT 53
A39660
heat shock protein SIS1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N2879; protein YNL007c
C;Species: Saccharomyces cerevisiae
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A39660; S62918; S17003; S19042
R;Luke, M.M.; Sutton, A.; Arndt, K.T.
J. Cell Biol. 114, 623-638, 1991

A;Title: Characterization of SIS1, a Saccharomyces cerevisiae homologue of bacterial dna
A;Reference number: A39660; MUID:91332100; PMID:1714460
A;Accession: A39660
A;Molecule type: DNA
A;Residues: 1-352 <LUK>
A;Cross-references: UNIPROT:P25294; GB:X58460; NID:g4473; PIDN:CAA41366.1; PID:g4474
R;Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62916
A;Accession: S62918
A;Molecule type: DNA
A;Residues: 1-352 <DOI>
A;Cross-references: EMBL:Z71283; NID:gl301823; PIDN:CAA95866.1; PID:gl301824; MIPS:YNL00
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:SIS1
A;Cross-references: SGD:S0004952; MIPS:YNL007c
A;Map position: 14L
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: dimer; DNA binding; heat shock; stress-induced protein
F;6-68/Domain: dnaJ amino-terminal homology <DNJ>
F;141-166/Region: glycine/methionine-rich

Query Match 54.3%; Score 44; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYG 10
Db 59 OKREIYDQYG 68

RESULT 54
F81333
chaperone DnaJ Cj1260c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: F81333
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: F81333
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <PAR>
A;Cross-references: UNIPROT:O85213; GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB7351
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: dnaJ; Cj1260c
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 54.3%; Score 44; DB 2; Length 373;
Best Local Similarity 53.3%; Pred. No. 5.1;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAF 15
Db 60 EKRAIYDRYGHKALK 74

RESULT 55
T09709
ADP,ATP carrier protein CANT1 - upland cotton
N;Alternate names: adenine nucleotide translocator 1
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09709
R;Shin, H.; Brown, R.M.
submitted to the EMBL Data Library, June 1997
A;Reference number: Z16832
A;Accession: T09709

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-386 <SHI>
A;Cross-references: UNIPROT:O22342; EMBL:AF006489; NID:g2463663; PID:g2463664
A;Experimental source: strain Texas marker1; fiber
C;Genetics:
A;Gene: CANT1
C;Function:
A;Description: catalyzes the exchange of ADP and ATP
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
P;188-282/Domain: ADP,ATP carrier protein repeat homology <ACR>

Query Match 54.3%; Score 44; DB 2; Length 386;
Best Local Similarity 53.3%; Pred. No. 5.3;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
:|||||:|:|:
Db 40 QKRAAYGNYSNALQ 54
:|||||:|:|:

RESULT 56
T44957
heat shock protein dnaJ [similarity] - Halobacterium salinarum (ATCC 33170)
N;Alternate names: 40K chaperone; 40K heat shock protein
C;Species: Halobacterium salinarum
A;Variety: ATCC 33170
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44957
R;Bustard, K.; Gupta, R.S.
J. Mol. Evol. 45, 193-205, 1997
A;Title: The sequences of heat shock protein 40 (DnaJ) homologs provide evidence for a
A;Reference number: 222880; MUID:97383250; PMID:9236279
A;Accession: T44957
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-389 <BUS>
A;Cross-references: UNIPROT:O34135; EMBL:U93357; PIDN:AAB96891.1
A;Experimental source: ATCC 33170
A;Note: the source is designated as Halobacterium cutirubrum
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;4-68/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 389;
Best Local Similarity 53.3%; Pred. No. 5.3;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
:|||||:|:|:
Db 59 ETRQQYDQLGHERFE 73
:|||||:|:|:

RESULT 57
E84207
heat shock protein [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84207
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Dantels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: E84207
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-391 <STO>
A;Cross-references: UNIPROT:Q9HRY3; GB:A8004437; NID:g10580095; PIDN:AAG19025.1; GSPDB:G
C;Genetics:

A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 54.3%; Score 44; DB 2; Length 391;
Best Local Similarity 53.3%; Pred. No. 5.3;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
:|||||:|:|:
Db 59 ETRQQYDQLGHERFE 73
:|||||:|:|:

RESULT 58
S33312
dnaJ protein - leek (fragment)
C;Species: Allium porrum (leek)
C;Date: 06-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S33312; MUID:93265942; PMID:8495747
R;Bessoule, J.J.
FEBS Lett. 323, 51-54, 1993
A;Title: Occurrence and sequence of a DnaJ protein in plant (Allium porrum) epidermal
A;Reference number: S33312
A;Accession: S33312
A;Molecule type: mRNA
A;Residues: 1-397 <BES>
A;Cross-references: UNIPROT:Q03363; EMBL:X69436; NID:g16086; PIDN:CAA49211.1; PID:g1608
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;1-53/Domain: dnaJ amino-terminal homology (fragment) <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 397;
Best Local Similarity 53.3%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
:|||||:|:|:
Db 44 EKREIYDQYGEDALK 58
:|||||:|:|:

RESULT 59
S35581
dnaJ protein homolog DnaJ-1 - cucumber
C;Species: Cucumis sativus (cucumber)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S35581; S31414
R;Preisig-Mueller, R.; Kindl, H.
Arch. Biochem. Biophys. 305, 30-37, 1993
A;Title: Plant dnaJ homologue: molecular cloning, bacterial expression, and expression
A;Reference number: S35581; MUID:93343632; PMID:8342953
A;Accession: S35581
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-413 <PRE1>
A;Cross-references: UNIPROT:Q04960; EMBL:X67695
R;Preisig-Mueller, R.; Kindl, H.
submitted to the EMBL Data Library, August 1992
A;Description: Plant equivalent of a nuclear localization sequence-binding protein. Hig
A;Reference number: S31414
A;Accession: S31414
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223, 'V', 225-239, 'A', 241-302, 'P', 304-377, 379-380, 'V', 381-413 <PRE2>
A;Cross-references: EMBL:X67695; NID:g18259; PIDN:CAA47925.1; PID:g18260
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;12-73/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 413;
Best Local Similarity 53.3%; Pred. No. 5.6;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
:|||||:|:|:

Db 64 EKREIYDQYGEDALK 78

RESULT 60

JQ2142

Chaperone ANU1 protein - Atriplex nummularia

C:Species: Atriplex nummularia

C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C:Accession: JQ2142

R:Zhu, J.K.; Shi, J.; Bressan, R.A.; Hasegawa, P.M.

Plant Cell 5, 341-349, 1993

A:Title: Expression of an Atriplex nummularia gene encoding a protein homologous to the

A:Reference number: JQ2142; M0ID:93222693; PMID:8467224

A:Accession: JQ2142

A:Molecule type: mRNA

A:Residues: 1-417 <ZHU>

A:CROSS-references: UNIPROT:P43644; GB:I09124

C:Comment: This protein is involved in protein folding and is observed as heat shock pro

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: molecular chaperone

F:13-74/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 417;

Best Local Similarity 53.3%; Pred. No. 5.7;

Matches 8; Conservative 2; Mismatches 2; Indels 5; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

Db 65 EKREIYDQYGEDALK 79

RESULT 61

T07371

dnaJ protein homolog - potato

C:Species: Solanum tuberosum (potato)

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004

C:Accession: T07371

R:Leggiewie, G.; Braun, H.P.

Plant Physiol. 117, 1127, 1998

A:Title: A cDNA from potato with homology to DnaJ is identical to a hitherto unidentified

A:Reference number: Z15992

A:Accession: T07371

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-419 <LEG>

A:CROSS-references: UNIPROT:Q43177; EMBL:X94301; NID:g1125690; PIDN:CAA63965.1

A:Experimental source: tissue type leaf

C:Genetics:

A:Gene: dnaJ

A>Note: induced upon tuberization

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: molecular chaperone

F:13-74/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 419;

Best Local Similarity 53.3%; Pred. No. 5.7;

Matches 8; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

Db 65 EKREIYDQYGEDALK 79

RESULT 62

T01643

DnaJ protein homolog ZMDJ1 - maize

C:Species: Zea mays (maize)

C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004

C:Accession: T01643

R:Baszczynski, C.L.; Barbour, E.; Zeka, B.; Maddock, S.E.; Swenson, J.L.

Maydica 42, 189-201, 1997

A:Title: Characterization of a genomic clone for a maize DnaJ-related gene, ZmdJ1, and e

A:Reference number: Z14364

A:Accession: T01643

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-419 <BAS>

A:CROSS-references: UNIPROT:O65160; EMBL:AF053468; NID:g2984708; PIDN:AAC08009.1; PID:g2984708

C:Genetics:

A:Gene: mdj1

A:Introns: 50/3; 105/1; 153/2; 245/3; 312/1

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: heat shock; molecular chaperone

F:13-74/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 419;

Best Local Similarity 53.3%; Pred. No. 5.7;

Matches 8; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

Db 65 EKREIYDQYGEDALK 79

RESULT 63

S71199

dnaJ protein homolog atj3 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C:Accession: S71199

R:Zhou, R.; Kroczyńska, B.; Miernyk, J.A.

submitted to the EMBL Data Library, March 1995

A:Description: AtJ3, an Arabidopsis thaliana homologue of the Escherichia coli DnaJ.

A:Reference number: S71199

A:Accession: S71199

A:Molecule type: mRNA

A:Residues: 1-420 <ZHO>

A:CROSS-references: UNIPROT:Q42530; EMBL:U22340; NID:gi872162; PIDN:AAB49030.1; PID:g72162

C:Genetics:

A:Gene: atj3

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

F:14-75/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 420;

Best Local Similarity 53.3%; Pred. No. 5.7;

Matches 8; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

Db 66 EKREIYDQYGEDALK 80

RESULT 64

T49127

dnaJ protein homolog atj3 - Arabidopsis thaliana

N:Alternate names: protein F26G5.60

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C:Accession: T49127

R:P'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.;

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z25017

A:Accession: T49127

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-420 <DAN>

A:CROSS-references: UNIPROT:O22663; EMBL:AL33814; GSPDB:GN00061; ATSP:F26G5.60

A:Experimental source: cultivar Columbia; BAC clone F26G5

C:Genetics:

A:Gene: ATSP:F26G5.60

A:Map position: 3

A:Introns: 51/3; 107/1; 153/2; 245/3; 312/1

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

F:14-75/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 420;

Best Local Similarity 53.3%; Pred. No. 5.7;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAPE 15
DB 66 EKREIYDQYGEDALK 80

RESULT 65
T09601
DnaJ protein homolog - alfalfa (fragment)
C/Species: Medicago sativa (alfalfa)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T09601
R/Frugis, G.
submitted to the EMBL Data Library, April 1996
A/Description: Isolation of an alfalfa DnaJ-like gene and a Y13 proteasome subunit homolog
A/Reference number: Z16763
A/Accession: T09601
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-170 <FRU>
A/Cross-references: UNIPROT:O24075; EMBL:Z71997
A/Experimental source: variety Rangelsander; non-embryogenic callus
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C/Keywords: molecular chaperone

Query Match 53.1%; Score 43; DB 2; Length 170;
Best Local Similarity 46.7%; Pred. No. 3.4;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAPE 15
DB 4 EKRESYDQYGEDALK 18

RESULT 66
JC7933
spermatogenic cell-specific DnaJ-like protein, MFSJ1 protein - Japanese macaque
C/Species: Macaca fuscata (Japanese macaque)
C/Date: 22-Jun-2003 #sequence_revision 22-Jun-2003 #text_change 07-Jul-2003
C/Accession: JC7933
R/Yu, S.S.; Takenaka, O.
Biochem. Biophys. Res. Commun. 301, 443-449, 2003
A/Title: Molecular cloning, structure, and testis-specific expression of MFSJ1, a member of the DnaJ family
A/Reference number: JC7933; MUID:22452769; PMID:12565881
A/Accession: JC7933
A/Molecule type: mRNA
A/Residues: 1-242 <YUA>
A/Cross-references: DDBJ:AB095737
C/Comment: This protein is a testis-specific DnaJ-like protein. It acts together with the DnaJ family proteins to regulate spermatogenesis.
C/Genetics:
A/Gene: mfsj1
C/Keywords: DnaJ-like protein; spermatogenesis; testis-specific

Query Match 53.1%; Score 43; DB 2; Length 242;
Best Local Similarity 53.3%; Pred. No. 4.9;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAPE 15
DB 60 KKRVDYDRYGEAGAE 74

RESULT 67
T08563
dnaJ-related protein T22F8.50 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T08563
R/Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May
submitted to the Protein Sequence Database, May 1999

A/Reference number: Z16442
A/Accession: T08563
A/Molecule type: DNA
A/Residues: 1-345 <BEV>
A/Cross-references: UNIPROT:Q9T024; EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.50
A/Experimental source: cultivar Columbia; BAC clone T22F8
C/Genetics:
A/Gene: ATSP:T22F8.50
A/Map position: 4
A/Introns: 29/3; 49/3; 77/2; 132/3; 176/1; 229/1; 286/3; 313/3
F:6-71/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 53.1%; Score 43; DB 2; Length 345;
Best Local Similarity 70.0%; Pred. No. 7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGH 10
DB 62 EKRTAYDKYG 71

RESULT 68
B72327
dnaJ protein - Thermotoga maritima (strain MSB8)
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: B72327
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, J.R.; Nelson, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D. C.M.
Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: B72327
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-369 <ARN>
A/Cross-references: UNIPROT:Q9WZV3; GB:AE001751; GB:AE000512; NID:g4981371; PIDN:AAD359
A/Experimental source: strain MSB8
C/Genetics:
A/Gene: TW0849
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F:7-73/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 53.1%; Score 43; DB 2; Length 369;
Best Local Similarity 63.6%; Pred. No. 7.5;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGH 11
DB 64 QKRAWYDRFGY 74

RESULT 69
T06102
heat shock protein T5J17.130, dnaJ-type - Arabidopsis thaliana
N/Alternate names: protein T5J17.130
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06102
R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, March 1999
A/Reference number: Z15184
A/Accession: T06102
A/Molecule type: DNA
A/Residues: 1-396 <BEV>
A/Cross-references: UNIPROT:Q9SMQ9; EMBL:AL035708; GSPDB:GN00062; ATSP:T5J17.130
A/Experimental source: cultivar Columbia; BAC clone T5J17
C/Genetics:
A/Gene: ATSP:T5J17.130
A/Map position: 4
A/Introns: 33/3; 53/1; 67/2; 83/3; 111/3
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: heat shock; stress-induced protein
F:34-98/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 53.1%; Score 43; DB 2; Length 396;
Best Local Similarity 58.3%; Pred. No. 8.1;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
:|:|:|:|:|
DB 89 EKRSYLDYRGEA 100

RESULT 70

T48660
heat shock protein dnaJ [validated] - Campylobacter jejuni

N:Alternate names: chaperone DnaJ

C:Species: Campylobacter jejuni

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C:Accession: T48660

R:Konkel, M.E.; Kim, B.J.; Klena, J.D.; Young, C.R.; Ziprin, R.

Infect. Immun. 66, 3666-3672, 1998

A:Title: Characterization of the thermal stress response of campylobacter jejuni.

A:Reference number: Z24513; MUID:98339866; PMID:9673247

A:Accession: T48660

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-372 <KON>

A:Cross-references: UNIPROT:O85213; EMBL:AF052661; NID:g3435158; PIDN:AAC32328.1; PID:g3

A:Experimental source: strain F38011

C:Genetics:

A:Gene: dnaJ

C:Function:

A:Description: aids in bacteriophage replication [validated, MUID:98339866]

A>Note: elevated expression after heat shock

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: heat shock; molecular chaperone

F:4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 51.9%; Score 42; DB 2; Length 372;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
:|:|:|:|:|
DB 60 EKRAIYDRYG 69

RESULT 71

S73459
heat shock protein DnaJ - Mycoplasma pneumoniae (strain ATCC 29342)

N:Alternate names: hypothetical protein D12_orf390

C:Species: Mycoplasma pneumoniae

A:Variety: ATCC 29342

C:Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S73459

R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A:Reference number: S73327; MUID:97105885; PMID:8948633

A:Accession: S73459

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-390 <HIM>

A:Cross-references: UNIPROT:P78004; EMBL:AE000015; GB:U00089; NID:g1673779; PIDN:AAB9578

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C:Genetics:

A:Gene: dnaJ

A:Genetic code: SGCS

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

F:7-77/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 51.9%; Score 42; DB 2; Length 390;
Best Local Similarity 54.5%; Pred. No. 12;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGH 11
:|:|:|:|:|
DB 68 EKRCMYDRFGH 78

RESULT 72

D81683

dnaJ protein TC0619 [imported] - Chlamydia muridarum (strain Nigg)

C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: D81683

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: D81683

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-392 <TET>

A:Cross-references: UNIPROT:Q9PK53; GB:AE002330; GB:AE002160; NID:g7190649; PIDN:AAF3945

A:Experimental source: strain Nigg (MoPn)

C:Genetics:

A:Gene: TC0619

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 51.9%; Score 42; DB 2; Length 392;

Best Local Similarity 70.0%; Pred. No. 12;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
:|:|:|:|:|
DB 58 QKRESYDRYG 67

RESULT 73

H71526

probable heat shock protein J - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C:Accession: H71526

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis

A:Reference number: A71570; MUID:99000809; PMID:9784136

A:Accession: H71526

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-392 <ARN>

A:Cross-references: UNIPROT:O84345; GB:AE001307; GB:AE001273; NID:g3328757; PIDN:AAC6793

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: dnaJ

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

F:2-67/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 51.9%; Score 42; DB 2; Length 392;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
:|:|:|:|:|
DB 58 QKRESYDRYG 67

RESULT 74

T43929

DnaJ protein homolog [imported] - Salix gilgiana

C:Species: Salix gilgiana

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T43929

R;Putamura, N.; Ishii-Minami, N.; Hayaehida, N.; Shinohara, K.
Plant Cell Physiol. 40, 524-531, 1999
A;Title: Expression of DnaJ homologs and Hep70 in the Japanese Willow (*Salix gilgiana* Se
A;Reference number: Z22726; MUID:99356782; PMID:10427775
A;Accession: T43929
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-423 <FUT>
A;Cross-references: UNIPROT:Q9SYX7; EMBL:AB003137; PIDN:BAA76883.1
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;13-74/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 51.9%; Score 42; DB 2; Length 423;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db 66 KREYDQYGEDALK 79

RESULT 75
S42091
Tid(56) protein - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42091
R;Kurzik-Dumke, U.; Gundacker, D.; Rentrop, M.; Gateff, E.
submitted to the EMBL Data Library, February 1994
A;Description: Tumor suppression in *Drosophila* is causally related to the function of th
A;Reference number: S42091
A;Accession: S42091
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-518 <KUR>
A;Cross-references: UNIPROT:Q27237; EMBL:X77822; NID:g2511642; PID:g456627
C;Genetics:
A;Gene: FlyBase:l(2)tid
A;Cross-references: FlyBase:FBgn0002174
A;Introns: 443/2
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;63-128/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 51.9%; Score 42; DB 2; Length 518;
Best Local Similarity 61.5%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KRAAYDQYGHAA 13
Db 119 QKRREYDTYGQTA 131

RESULT 76
T12472
Hypothetical protein DKFZp564F1862.1 - human
C;Species: *Homo sapiens* (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12472
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17526
A;Accession: T12472
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223 <BLU>
A;Cross-references: UNIPROT:Q9UBS3; EMBL:AL080081
A;Experimental source: fetal brain; clone DKFZp564F1862
C;Genetics:
A;Note: DKFZp564F1862.1
F;26-90/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 223;
Best Local Similarity 53.8%; Pred. No. 10;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFP 14
Db 82 RRKEYDTLGHSAF 94

RESULT 77
A97106
Response regulator (Chey-like receiver domain and DNA-binding HTH domain) [imported] -
C;Species: *Clostridium acetobutylicum*
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 15-Sep-2003
C;Accession: A97106
R;Nolling, J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
; Daly, M.J.; Bennett, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A97106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <KUR>
A;Cross-references: GB:AB001437; PIDN:AAK79636.1; PID:g15024631; GSPDB:GN00168
C;Experimental source: *Clostridium acetobutylicum* ATCC824
C;Genetics:
A;Gene: CAC1670
C;Superfamily: response regulator with LysR DNA-binding domain, Algr/VirK/ComE type; r

Query Match 50.6%; Score 41; DB 2; Length 253;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 AYDQYGHAAFE 15
Db 84 AYDKYAAVAAPF 94

RESULT 78
T39146
Hypothetical protein SPAC8C9.09c - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39146
R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21748
A;Accession: T39146
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-302 <OLI>
A;Cross-references: UNIPROT:O14278; EMBL:Z99168; PIDN:CAB16297.1; GSPDB:GN00066; SPDB:5
A;Experimental source: strain 972h-; cosmid c8C9
C;Genetics:
A;Gene: SPDB:SPAC8C9.09c
A;Map position: 1

Query Match 50.6%; Score 41; DB 2; Length 302;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFP 14
Db 154 RXKALSKLGHAPF 167

RESULT 79
E86237
protein F14N23.23 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86237
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86237
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <STO>
A:Cross-references: UNIPROT:Q9SY77; GB:AE005172; NID:g4914337; PIDN:AAD32885.1; GSPDB:GN
A:Gene: F14N23.23
C:Genetics: 1
A:Map position: 1
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 50.6%; Score 41; DB 2; Length 349;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYG 10
|:|:|:|:|:|:|
Db 61 QRRQIYDQYG 70

RESULT 80
G71831
co-chaperone with dnaK - *Helicobacter pylori* (strain J99)
C:Species: *Helicobacter pylori*
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: G71831
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: G71831
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-369 <ARN>
A:Cross-references: UNIPROT:Q9ZJ02; GB:AE001548; GB:AE001439; NID:g4155845; PIDN:AAD0682
A:Experimental source: strain J99
C:Genetics:
A:Gene: dnaJ.2
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 369;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDQYG 10
|:|:|:|:|:|:|
Db 60 KKGALYDRYG 69

RESULT 81
D64686
co-chaperone and heat shock protein - *Helicobacter pylori* (strain 26695)
C:Species: *Helicobacter pylori*
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: D64686
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujiki, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A:Reference number: A64520; MUID:9739467; PMID:9252185

A:Accession: D64686
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-369 <TOM>
A:Cross-references: UNIPROT:O25890; GB:AE000634; GB:AE000511; NID:g2314489; PIDN:AAD0837
C:Genetics:
A:Start codon: GTG
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 369;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDQYG 10
|:|:|:|:|:|:|
Db 60 KKRALYDRYG 69

RESULT 82
S21313
ADP, ATP carrier protein - *Arabidopsis thaliana* (fragment)
N:Alternate names: adenine nucleotide translocator
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S21313
R:Saint-Gully, A.; Poh-Yam, L.; Chevalier, C.; Yamaguchi, J.; Akazawa, T.
submitted to the EMBL Data Library, April 1992
A:Reference number: S21313
A:Accession: S21313
A:Molecule type: mRNA
A:Residues: 1-379 <SAI>
A:Cross-references: UNIPROT:P31167; EMBL:X65549; NID:g16174; PIDN:CAA46518.1; PID:g16175
C:Genetics:
A:Gene: ANTI
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C:Keywords: duplication; mitochondrion; transmembrane protein
F;75-170/Domain: ADP, ATP carrier protein repeat homology <ACPI>
F;180-275/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F;281-369/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 50.6%; Score 41; DB 2; Length 379;
Best Local Similarity 46.7%; Pred. No. 18;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
|:|:|:|:|:|:|
Db 36 QRHATYGNYSNAAFQ 50

RESULT 83
S55900
DNAJ-like protein homolog - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S55900
R:Park, S.K.; Chon, S.K.; Yoo, H.S.
Biochim. Biophys. Acta 1262, 87-90, 1995
A:Title: A cDNA of *Schizosaccharomyces pombe* encoding a homologue of DnaJ-like protein.
A:Reference number: S55900; MUID:95290501; PMID:7772606
A:Accession: S55900
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <PAR>
A:Cross-references: UNIPROT:Q09912; EMBL:L37753; NID:g576932; PIDN:AAA74732.1; PID:g95932
C:Genetics:
A:Gene: psi
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;6-68/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 379;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
Db 59 QRRKLYDQYG 68

RESULT 84

T41633
psi protein - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R/McDougal, R.M.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A/Reference number: Z22005
A/Accession: T41633
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-379 <MCD>
A/Cross-references: UNIPROT:Q09912; EMBL:AL109850; PIDN:CAB52880.1; GSPDB:GN00068; SPDB:
A/Experimental source: strain 972h; cosmid c830
C/Genetics:
A/Gene: SPDB:SPCC830.07C
A/Map position: 3
C/Species: Schizosaccharomyces pombe
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F/6-68/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 379;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
Db 59 QRRKLYDQYG 68

RESULT 85

G84611
probable DnaJ protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: G84611
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: G84611
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-391 <STO>
A/Cross-references: UNIPROT:Q9SJZ7; GB:AB002093; NID:94544454; PIDN:AAD22362.1; GSPDB:GN
C/Genetics:
A/Gene: At2g22360
A/Map position: 2
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 50.6%; Score 41; DB 2; Length 391;
Best Local Similarity 40.0%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
Db 90 EKSLYDQYGEAGLK 104

RESULT 86

S42031
LDJ2 protein - leek
C/Species: Allium porrum (leek)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S42031

R/Bessoule, J.J.; Testet, B.; Cassagne, C.
submitted to the EMBL Data Library, February 1994
A/Reference number: S42031
A/Accession: S42031
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-418 <BES>
A/Cross-references: UNIPROT:P42824; EMBL:X77632; NID:9454913; PIDN:CAA54720.1; PID:9454
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F/13-74/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 418;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
Db 65 EKREIYDQYG 74

RESULT 87

T09338
DnaJ-like protein MeJ1 - alfalfa
C/Species: Medicago sativa (alfalfa)
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C/Accession: T09338
R/Frugis, G.; Mele, G.; Giannino, D.; Mariotti, D.
submitted to the EMBL Data Library, June 1998
A/Description: Isolation and characterization of a DnaJ-like gene from alfalfa.
A/Reference number: Z16649
A/Accession: T09338
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-423 <FRU>
A/Cross-references: UNIPROT:O24074; EMBL:AF069507; NID:G3202019; PID:G3202020
C/Genetics:
A/Gene: MeJ1
A/Int-ns: 51/3; 108/1; 155/2; 200/1; 247/3; 314/1
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F/4-15/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 423;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
Db 66 EKRELYDQYGHAAPE 80

RESULT 88

T41362
hypothetical protein SPCC4G3.14 - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 05-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T41362
R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, March 1998
A/Reference number: Z21918
A/Accession: T41362
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-528 <WOO>
A/Cross-references: UNIPROT:P87239; EMBL:Z97052; PIDN:CAB09769.1; GSPDB:GN00068; SPDB:
A/Experimental source: strain 972h; cosmid c4G3
C/Genetics:
A/Gene: SPDB:SPCC4G3.14
A/Map position: 3
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F/86-150/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 528;
Best Local Similarity 46.7%; Pred. No. 25;

Qy 5 AYDQYGH 11
|||:||||

Db 46 AYDEYGH 52

RESULT 93

3-isopropylmalate dehydrogenase NM1031 [imported] - Neisseria meningitidis (strain MC58)

C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: E81130

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vitti, A.; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: AB1000; MUID:20175755; PMID:10710307

A;Accession: E81130

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-356 <TET>

A;Cross-references: UNIPROT:Q9JZ19; GB:AE002453; NID:g7226261; PIDN:AAF4143

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NM1031

C;Superfamily: 3-isopropylmalate dehydrogenase

Query Match 49.4%; Score 40; DB 2; Length 356;

Best Local Similarity 85.7%; Pred. No. 25;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AYDOYGH 11

Db 46 AYDEYGH 52

RESULT 94

E81836

probable 3-isopropylmalate dehydrogenase (EC 1.1.1.85) NMA1456 [imported] - Neisseria meningitidis

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: E81836

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jogle, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: AB1775; MUID:2022556; PMID:10761919

A;Accession: E81836

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-356 <PAR>

A;Cross-references: UNIPROT:Q9JU79; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB8469

A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: NMA1454; NMA1456

C;Superfamily: 3-isopropylmalate dehydrogenase

C;Keywords: oxidoreductase

Query Match 49.4%; Score 40; DB 2; Length 356;

Best Local Similarity 85.7%; Pred. No. 25;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AYDOYGH 11

Db 46 AYDEYGH 52

RESULT 95

D95350

probable transmembrane transport protein Sma1301 [imported] - Sinorhizobium meliloti (strain 1021)

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: D95350

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: D95350

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-385 <KUR>

A;Cross-references: UNIPROT:Q92Z04; GB:AE006469; PIDN:AAK65366.1; PID:g14523826; GSPDB: A;Experimental source: strain 1021, megaplasmid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, M.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

C;Genetics:

A;Gene: Sma1301

A;Genome: plasmid

C;Superfamily: probable antibiotic resistance protein yybF

Query Match 49.4%; Score 40; DB 2; Length 385;

Best Local Similarity 57.1%; Pred. No. 27;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAF 14

Db 199 QKRAAYDQYGHAAF 212

RESULT 96

T18661

hypothetical protein B0035.14 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T18661

R;White, S. Submitted to the EMBL Data Library, May 1996

A;Reference number: Z19002

A;Accession: T18661

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-401 <WIL>

A;Cross-references: UNIPROT:Q17438; EMBL:Z73102; PIDN:CRA97416.1; GSPDB:GN00022; CESP: B0035

A;Experimental source: clone B0035

C;Genetics:

A;Gene: CESP:B0035.14

A;Map position: 4

A;Introns: 22/3; 47/1; 180/1; 233/1; 310/2; 365/1

Query Match 49.4%; Score 40; DB 2; Length 401;

Best Local Similarity 66.7%; Pred. No. 28;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAA 13

Db 193 KRRQYDQYGHAA 204

RESULT 97

T39658

probable mitochondrial protein import protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C;Accession: T39658

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M. submitted to the EMBL Data Library, October 1998

A;Reference number: Z21868

A;Accession: T39658

A;Status: preliminary

A:Molecule type: DNA
A:Residues: 1-407 <LYN>
A:Cross-references: UNIPROT:O74752; EMBL:AL031856; PIDN:CAA21305.1; GSPDB:GN000067; SPDB:
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: mitochondrion
F:6-68/Domain: dnaJ amino-terminal homology <DNJ>
Query Match 49.4%; Score 40; DB 2; Length 407;
Best Local Similarity 40.0%; Pred. No. 28;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 OKRAAYDQYGHAAFE 15
:|||||:|:
Db 59 EKRAYDREFGEGLQ 73
:|||||:|:
RESULT 98
F75396
dnaJ protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: F75396
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Ma
; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: F75396
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-420 <WHI>
A:Cross-references: GB:AE001987; GB:AE000513; NID:g6459180; PIDN:AAF10994.1; PID:g645918
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRI424
A:Map position: 1
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
Query Match 49.4%; Score 40; DB 2; Length 420;
Best Local Similarity 58.3%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 OKRAAYDQYGHCA 12
:|||||:|:
Db 101 EKRAYDREFGSA 112
:|||||:|:
RESULT 99
A64222
heat shock protein dnaJ homolog MG200 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: A64222; T09695
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
; C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: A64222
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-601 <TIGR>
A:Cross-references: UNIPROT:P47442; GB:U39697; GB:I43967; NID:g1045878; PID:g1045885; TI
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
; M.; Fuhrmann, J.L.; Nguyen, D.T.; Utterback, T.; Saudek, D.M.; Phillips, C.A.; Merrick
submitted to the EMBL Data Library, October 1998
A:Reference number: Z16818

A:Accession: T09695
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-601 <FRA>
A:Cross-references: EMBL:U39699; NID:g3844790; PID:g3844797
A:Experimental source: isolate G37
C:Genetics:
A:Gene: MG200
A:Genetic code: SGC3
C:Superfamily: Mycoplasma heat shock protein dnaJ homolog MG200; dnaJ amino-terminal hom
C:Keywords: molecular chaperone
F:7-71/Domain: dnaJ amino-terminal homology <DNJ>
Query Match 49.4%; Score 40; DB 1; Length 601;
Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 OKRAAYDQYG 10
:|||||:|:
Db 62 KKRANYDKYG 71
:|||||:|:
RESULT 100
A83182
hypothetical protein PA3713 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: A83182
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83182
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-620 <STO>
A:Cross-references: UNIPROT:Q9HXS8; GB:AE004790; GB:AE004091; NID:g9949873; PIDN:AAG0710
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3713
Query Match 49.4%; Score 40; DB 2; Length 620;
Best Local Similarity 58.3%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 4 AAYDQYGHAAFE 15
:|||||:|:
Db 599 AAWDAYAHAAID 610
:|||||:|:
Search completed: September 2, 2005, 20:55:40
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 2, 2005, 20:44:11 ; Search time 56 Seconds
(without alignments)
137.164 Million cell updates/sec

Title: US-09-616-247-4

Perfect score: 81

Sequence: 1 QKRAAYDQYGHAAPE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	372	2 QN8Y3	Q7N8Y3 photorhabdu
2	81	100.0	375	1 DNAJ_ECOLI	P08622 escherichia
3	81	100.0	376	2 Q7UD1	Q7UD1 shigella fl
4	81	100.0	376	2 Q8FLC5	Q8FLC5 escherichia
5	81	100.0	376	2 Q8XA65	Q8XA65 escherichia
6	81	100.0	377	1 DNAJ_HABDU	P48208 haemophilus
7	81	100.0	378	1 DNAJ_SALTY	Q60004 salmonella
8	81	100.0	379	2 Q8L3D3	Q8L3D3 colwellia m
9	81	100.0	379	2 Q6B8S9	Q6B8S9 yersinia ps
10	81	100.0	379	2 Q75WD2	Q75WD2 acetobacter
11	81	100.0	379	2 Q8ZIM6	Q8ZIM6 yersinia pe
12	81	100.0	379	2 Q6D0B8	Q6D0B8 erwinia pe
13	81	100.0	382	1 DNAJ_HABIN	P43735 haemophilus
14	81	100.0	386	2 Q83MH4	Q83MH4 shigella fl
15	78	96.3	375	1 DNAJ_ACTAC	P77866 actinobacil
16	78	96.3	380	2 Q6LUJ6	Q6LUJ6 photobacter
17	78	96.3	381	1 DNAJ_VIBCH	Q34242 vibrio chol
18	78	96.3	381	2 Q87RX2	Q87RX2 vibrio para
19	78	96.3	381	2 Q8DF67	Q8DF67 vibrio vuln
20	78	96.3	385	1 DNAJ_VIBHA	Q87385 vibrio harv
21	78	96.3	386	2 Q7MN84	Q7MN84 vibrio vuln
22	78	96.3	389	2 Q65U54	Q65U54 manheimia
23	77	95.1	234	1 DNAJ_RHILE	Q33529 rhizobium l
24	77	95.1	331	2 Q93S23	Q93S23 rhizobium t
25	77	95.1	379	2 Q92T07	Q92T07 rhizobium m
26	77	95.1	392	1 NOLC_RHIFR	P26508 rhizobium f
27	75	92.6	372	1 DNAJ_PASMU	Q9CMA2 pasteurella
28	75	92.6	377	1 DNAJ_BUCAI	Q32455 buchnera ap
29	74	91.4	378	1 DNAJ_BUCAP	Q8K9Y9 buchnera ap
30	73	90.1	373	1 DNAJ_NEIMA	P63968 neisseria m
31	73	90.1	373	1 DNAJ_NEIMB	P63969 neisseria m

32	73	90.1	1	DNAJ_BRUOV	Q05980 brucella ov
33	73	90.1	2	Q98DD2	Q98DD2 rhizobium l
34	73	90.1	3	DNAJ_AGR5	P50018 agrobacteri
35	73	90.1	377	1 DNAJ_BRUME	Q8Y677 brucella me
36	73	90.1	377	1 DNAJ_BRUSU	Q8FX11 brucella su
37	73	90.1	379	2 Q6RSN5	Q6RSN5 agrobacteri
38	73	90.1	380	2 Q6GIF8	Q6GIF8 bartonella
39	73	90.1	381	2 Q6G553	Q6G553 bartonella
40	72	88.9	379	1 DNAJ_RHOPA	Q6NCY3 rhodopsuendo
41	72	88.9	379	1 DNAJ_RHOSH	Q08356 rhodopsuendo
42	72	88.9	384	2 Q8R567	Q8R567 thermoaer
43	70	86.4	377	2 Q7VQL3	Q7VQL3 candidatus
44	70	86.4	379	1 DNAJ_PASHA	Q52065 pasteurella
45	70	86.4	383	1 DNAJ_BUCBP	Q89A07 buchnera ap
46	69	85.2	382	2 Q8KYX6	Q8KYX6 uncultured
47	69	85.2	384	1 DNAJ_RHOCA	Q52702 rhodobacter
48	68	84.0	370	1 DNAJ_ERYRH	Q05646 erysipeloth
49	68	84.0	377	1 DNAJ_BRAJA	P94319 bradyrhizob
50	67	82.7	371	1 DNAJ_METSS	Q9ZFC5 methylovoru
51	67	82.7	376	2 Q62HD6	Q62HD6 burkholderi
52	67	82.7	376	2 Q63R47	Q63R47 burkholderi
53	66	81.5	383	1 DNAJ_LACSK	Q87778 lactobacill
54	66	81.5	386	2 Q93R26	Q93R26 tetragenoco
55	65	80.2	374	2 Q8DQ6	Q8DQ6 wigglewort
56	64	79.0	370	1 DNAJ_RICPR	Q9ZD90 rickettsia
57	64	79.0	370	2 Q68XI3	Q68XI3 rickettsia
58	64	79.0	392	2 Q8RH03	Q8RH03 fusobacteri
59	64	79.0	393	2 Q7P753	Q7P753 fusobacteri
60	63	77.8	367	2 Q6SET1	Q6SET1 uncultured
61	63	77.8	369	2 Q6SGG2	Q6SGG2 uncultured
62	63	77.8	373	2 Q7WGI5	Q7WGI5 bordetella
63	63	77.8	376	1 DNJ2_AQUAE	Q66921 aquifex aeo
64	63	77.8	377	2 Q7W520	Q7W520 bordetella
65	63	77.8	379	1 DNAJ_LEGPN	P50025 legionella
66	63	77.8	385	2 Q7VVY3	Q7VVY3 bordetella
67	62	77.8	389	2 Q835R5	Q835R5 enterococcu
68	62	76.5	376	2 Q6VAY5	Q6VAY5 pseudomonas
69	62	76.5	377	1 DNAJ_PSEAE	Q9HV44 pseudomonas
70	62	76.5	380	2 Q87WP1	Q87WP1 pseudomonas
71	61	75.3	374	2 Q6F150	Q6F150 mesoplasma
72	61	75.3	394	2 Q8XIT1	Q8XIT1 clostridium
73	61	75.3	397	2 Q70WY6	Q70WY6 fusobacteri
74	60	74.1	373	2 Q7PAY0	Q7PAY0 rickettsia
75	60	74.1	373	2 Q92J37	Q92J37 rickettsia
76	60	74.1	375	2 Q8PMA9	Q8PMA9 xanthomonas
77	60	74.1	376	2 Q8APF2	Q8APF2 xanthomonas
78	60	74.1	376	2 Q8PAK8	Q8PAK8 xanthomonas
79	60	74.1	391	2 Q7UM96	Q7UM96 rhodopirell
80	59	72.8	374	1 DNAJ_CXBU	P42381 coxiella bu
81	59	72.8	375	2 Q7NXI1	Q7NXI1 chromobacte
82	59	72.8	380	2 Q8XW41	Q8XW41 ralatonia s
83	58	71.6	375	2 Q88DU3	Q88DU3 pseudomonas
84	58	71.6	379	1 DNAJ_LACLA	P35514 lactococcus
85	58	71.6	379	2 Q93Q66	Q93Q66 lactococcus
86	58	71.6	385	1 DNAJ_CAUCR	P22305 caulobacter
87	58	71.6	386	2 Q67S53	Q67S53 symbiobacte
88	58	71.6	414	2 Q7S1F9	Q7S1F9 neurospora
89	58	71.6	456	2 Q8LEU4	Q8LEU4 arabidopsis
90	57	70.4	188	2 Q8NK58	Q8NK58 paracoccidi
91	57	70.4	364	1 DNAJ_BORBU	P28616 borrelia bu
92	57	70.4	364	2 Q661A4	Q661A4 borrelia ga
93	57	70.4	367	2 Q6Q8U1	Q6Q8U1 uncultured
94	57	70.4	369	1 DNAJ_NITEU	Q06431 nitrosomona
95	57	70.4	371	2 Q634M8	Q634M8 bacillus ce
96	57	70.4	371	2 Q6MNG0	Q6MNG0 bdellovibri
97	57	70.4	371	2 Q730M2	Q730M2 bacillus ce
98	57	70.4	371	2 Q818F0	Q818F0 bacillus ce
99	57	70.4	371	2 Q81LS3	Q81LS3 bacillus an
100	57	70.4	371	2 Q6HDK8	Q6HDK8 bacillus th

ALIGNMENTS

```

RESULT 1
Q7N8Y3
ID Q7N8Y3 PRELIMINARY; PRT; 372 AA.
AC Q7N8Y3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Heat shock protein dnaJ (HSP40) (Chaperone protein).
GN Name=dnaJ; OrderedLocusNames=plu0580;
OS Phototrophic luminescens (subsp. laumondii);
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Phototrophic;
NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguer P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Beomare N., Dauchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Phototrophic
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; BX571860; CAE12875.1; -.
DR HSPB; P08622; 1BQZ.
DR PhotoList; plu0580; -.
DR GO; GO:0051082; F:unfolding protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXXG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXXG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 372 AA; 40820 MW; B2F36918CC6E9B1A CRC64;

Query Match 100.0%; Score 81; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 9,8e-06;
Matches 15; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 1 OKRAAYDQYGHAAFE 15
Db 61 OKRAAYDQYGHAAFE 75
|||||
|||||

RESULT 2
DnaJ_ECOLI
ID DnaJ_ECOLI STANDARD; PRT; 375 AA.
AC P08622;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Chaperone protein dnaJ (Heat shock protein J) (HSP40).

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GN Name=dnaJ; Synonyms=grpP; OrderedLocusNames=b0015;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
RX MEDLINE=86111849; PubMed=3003084;
RA Ohki M., Tamura F., Nishimura S., Uchida H.;
RT "Nucleotide sequence of the Escherichia coli dnaJ gene and
RT purification of the gene product.";
RL J. Biol. Chem. 261:1778-1781(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=86111850; PubMed=3003085;
RA Bardwell J.C.A., Tilly K., Craig E., King J., Zylicz M.,
RA Georgopoulos C.;
RT "The nucleotide sequence of the Escherichia coli K12 dnaJ+ gene. A
RT gene that encodes a heat shock protein.";
RL J. Biol. Chem. 261:1782-1785(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92334977; PubMed=1630901;
RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
RA Isono K., Mizobuchi K., Nakata A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of the
RT 0-2.4 min region.";
RL Nucleic Acids Res. 20:3305-3308(1992).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP POSSIBLE FUNCTION
RX MEDLINE=91187894; PubMed=1826368;
RA Liberek K., Marszalek J., Ang D., Georgopoulos C., Zylicz M.;
RT "Escherichia coli DnaJ and GrpE heat shock proteins jointly stimulate
RT ATPase activity of DnaK.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2874-2878(1991).
RN [6]
RP STRUCTURE BY NMR OF 1-107.
RX MEDLINE=96291434; PubMed=8764403; DOI=10.1006/jmbi.1996.0395;
RA Pellechia M., Szyperski T., Wall D., Georgopoulos C., Wuthrich K.;
RT "NMR structure of the J-domain and the Gly/Phe-rich region of the
RT Escherichia coli DnaJ chaperone.";
RL J. Mol. Biol. 260:236-250(1996).
RN [7]
RP STRUCTURE BY NMR OF 1-104.
RX MEDLINE=99224904; PubMed=10210198;
RA Huang K., Flanagan J.M., Prestegard J.H.;
RT "The influence of C-terminal extension on the structure of the 'J-
RT domain' in E. coli DnaJ.";
RL Protein Sci. 8:203-214(1999).
RN [8]
RP STRUCTURE BY NMR OF 130-208.
RX MEDLINE=20351465; PubMed=10891270; DOI=10.1006/jmbi.2000.3923;
RA Martinez-Yamout M., Legge G.B., Zhang O., Wright P.E., Dyson H.J.;
RT "Solution structure of the cysteine-rich domain of the Escherichia
RT coli chaperone protein DnaJ.";
RL J. Mol. Biol. 300:805-818(2000).
CC -!- FUNCTION: Interacts with dnaK to disassemble a protein complex at
CC the phage lambda origin of replication. Stimulates, jointly with
CC grpE, the ATPase activity of dnaK.
CC -!- COFACTOR: Binds 2 zinc ions per monomer.
CC -!- SUBUNIT: Homodimer.

```


CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: By heat shock under the control of the htrp regulatory
CC protein.
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M12544; AAA00009.1; -;
CC EMBL; M12565; AAA23693.1; -;
CC EMBL; D10483; BAB96590.1; -;
CC EMBL; U00096; AAC73126.1; -;
CC PIR; A92572; HHECDJ.
CC PDB; 1BQ0; NMR; @=1-103.
CC PDB; 1BQ2; NMR; @=1-77.
CC PDB; 1EXK; NMR; A=130-208.
CC PDB; 1XBL; NMR; @=1-107.
CC ECO2DBASE; H036.5; 6TH EDITION.
CC -----
CC EcoGene; EB0236; -;
CC EcoGene; EG10240; dnaJ.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; HSP40_DnaJ_pap.
CC InterPro; IPR003095; Hsp_DnaJ.
CC InterPro; IPR011031; Multihem_cyt.
CC Pfam; PF00226; DnaJ; 1.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW 3D-structure; Chapterone; Complete proteome; Direct protein sequencing;
KW DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT INIT MET 0 0
FT DOMAIN 2 71 J-domain.
FT DOMAIN 76 113 Gly-rich.
FT REPEAT 143 150 CXXCXGKG motif.
FT REPEAT 160 167 CXXCXGKG motif.
FT REPEAT 182 189 CXXCXGKG motif.
FT REPEAT 196 203 CXXCXGKG motif.
FT METAL 143 143 Zinc 1.
FT METAL 146 146 Zinc 1.
FT METAL 160 160 Zinc 1.
FT METAL 163 163 Zinc 2.
FT METAL 182 182 Zinc 2.
FT METAL 185 185 Zinc 2.
FT METAL 196 196 Zinc 1.
FT METAL 199 199 Zinc 1.
FT HELIX 5 8
FT TURN 9 10
FT TURN 13 14
FT HELIX 18 31
FT TURN 32 35
FT HELIX 36 38
FT TURN 41 42
FT HELIX 43 50
FT TURN 51 51
FT HELIX 52 56
FT HELIX 59 64
FT TURN 65 67
FT TURN 68 73
FT TURN 131 133
FT STRAND 140 142

FT HELIX 144 146
FT TURN 147 149
FT STRAND 151 151
FT STRAND 158 159
FT TURN 161 165
FT STRAND 168 173
FT TURN 174 175
FT STRAND 176 181
FT TURN 183 187
FT STRAND 190 191
FT STRAND 195 195
FT HELIX 197 199
FT TURN 200 201
FT STRAND 204 206
SQ SEQUENCE 375 AA; 40969 MW; 8DE1863CC0B8C3F CRC64;
Query Match 100.0%; Score 81; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 9.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OKRAAYDQYGHAAFE 15
DB 60 OKRAAYDQYGHAAFE 74
RESULT 3
ID Q7UDU1 PRELIMINARY; PRT; 376 AA.
AC Q7UDU1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chapterone with DnaJ; heat shock protein.
GN Name=dnaJ; OrderedLocusNames=S0015;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]_SEQUENCE FROM N.A.
RP STRAIN=2457T;
RC MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/JAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.P., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AS016978; AAP15561.1; -;
DR HSSP; P08622; 1EXK.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Heat shock.
SQ SEQUENCE 376 AA; 41072 MW; 1B354AC3F9844532 CRC64;
Query Match 100.0%; Score 81; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 9.9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

|||||

Db 61 QKRAAYDQYGHAAFE 75

RESULT 4

Q8FLCS PRELIMINARY; PRT; 376 AA.

AC Q8FLCS;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Chapterone protein dnaJ

GN Name=dnaJ; OrderedLocusNames=c0020;

OS Escherichia coli O6.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=217992;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O6:H1 / CF7073 / ATCC 700928;

RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/dnae.252529799;

RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

RT "Extensive mosaic structure revealed by the complete genome sequence

of uropathogenic Escherichia coli";

RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)

CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,

the ATPase activity of dnaK (By similarity).

CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the dnaJ family.

EMBL; AB016755; AA078520.1; -.

DR PIR; G85481; G85481.

DR PIR; G90630; G90630.

DR HSP; P08622; 1EXX.

DR GO; GO:0051082; F:unfolded protein binding; IEA.

DR GO; GO:0006260; P:DNA replication; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR GO; GO:0006457; P:response to unfolded protein; IEA.

DR InterPro; IPR000345; CytC_heme_BS.

DR InterPro; IPR002939; DnaJ_C.

DR InterPro; IPR001305; DnaJ_CXXCXGXG.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR008971; HSP40_DnaJ_pap.

DR InterPro; IPR003095; Hsp_DnaJ.

DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF01556; DnaJ_C; 1.

DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.

DR PRINTS; PS00190; CYTOCHROME_C; UNKNOWN_2.

DR PROSITE; PS00625; DnaJ_CXXCXGXG; 1.

DR PROSITE; PS00636; DnaJ_1; 1.

DR PROSITE; PS50076; DnaJ_2; 1.

DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.

KW Chaperone; Complete proteome; DNA replication; Heat shock;

KW Metal-binding; Repeat; Zinc.

SQ SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;

Query Match 100.0%; Score 81; DB 2; Length 376;

Best Local Similarity 100.0%; Pred. No. 9.9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

|||||

Db 61 QKRAAYDQYGHAAFE 75

RESULT 5

Q8XA65

Q8XA65 PRELIMINARY; PRT; 376 AA.

Q8XA65; Q7AHU4;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Chaperone with dnaJ, heat shock protein (DnaJ protein).

GN Name=dnaJ; OrderedLocusNames=EC90015, 20015;

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;

RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

RA Welch R.A., Blattner F.R.;

RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.;"

RL Nature 409:529-533(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RMD 050952 / EHEC;

RX MEDLINE=21156233; PubMed=11256796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RT "Complete genome sequence of enterohaemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.;"

RL DNA Res. 8:11-22(2001).

CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,

the ATPase activity of dnaK (By similarity).

CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the dnaJ family.

EMBL; AB005178; AB54315.1; -.

DR EMBL; AP002550; BAB33438.1; -.

DR PIR; G85481; G85481.

DR PIR; G90630; G90630.

DR HSP; P08622; 1EXX.

DR GO; GO:0051082; F:unfolded protein binding; IEA.

DR GO; GO:0006260; P:DNA replication; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR GO; GO:0006986; P:response to unfolded protein; IEA.

DR InterPro; IPR000345; CytC_heme_BS.

DR InterPro; IPR002939; DnaJ_C.

DR InterPro; IPR001305; DnaJ_CXXCXGXG.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR008971; HSP40_DnaJ_pap.

DR InterPro; IPR003095; Hsp_DnaJ.

DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF01556; DnaJ_C; 1.

DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.

DR PRINTS; PS00625; DnaJ_CXXCXGXG; 1.

DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.

DR PROSITE; PS00636; DnaJ_1; 1.

DR PROSITE; PS50076; DnaJ_2; 1.

DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.

KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc;

Complete proteome.

SQ SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;

Query Match 100.0%; Score 81; DB 2; Length 376;

Best Local Similarity 100.0%; Pred. No. 9.9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

|||||

Db 61 QKRAAYDQYGHAAFE 75

RESULT 6

ID DNAAJ_HAEDU : STANDARD; PRT; 377 AA.

AC P48208;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chaperone protein dnaJ.
 GN Name=dnaJ; OrderedLocuNames=HD0188;
 OS Haemophilus ducreyi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=730;
 RN [1]

SEQUENCE FROM N.A.

RP STRAIN=35000HP / ATCC 700724;
 RC Parsons L.M.;
 RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]

SEQUENCE FROM N.A.

RP STRAIN=35000HP / ATCC 700724;
 RA Munson R.S., Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
 RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
 RA "The complete genome sequence of Haemophilus ducreyi."
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL [1]
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the dnaJ family.
 CC -!- SIMILARITY: Contains 1 CR domain.
 CC -!- SIMILARITY: Contains 1 J domain.

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 CC or send an email to license@isb-sib.ch).
 CC -----

EMBL; U25996; AAA67299.1; --

EMBL; AE017151; AAP95181.1; --

HSSP; P08622; 1BQZ.

DR InterPro; IPR002939; DnaJ_C.

DR InterPro; IPR001305; DnaJ_CXXCXGKG.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR008971; HSP40 DnaJ_pap.

DR InterPro; IPR003095; Hsp DnaJ.

DR InterPro; IPR011031; Multitnaem_cyt.

DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF01556; DnaJ_C; 1.

DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.

DR PRINTS; PS00625; DnaJ_CXXCXGKG; 1.

DR PROSITE; PS00636; DnaJ_1; 1.

DR PROSITE; PS00076; DnaJ_2; 1.

DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.

KW Chaperone; Complete proteome; DNA replication; Heat shock;
 Metal-binding; Repeat; Zinc.

FT DOMAIN 3 72 J-domain.

FT DOMAIN 77 108 Gly-rich.

FT REPEAT 147 154 CXXCXGKG motif.

FT REPEAT 164 171 CXXCXGKG motif.

FT REPEAT 186 193 CXXCXGKG motif.

FT REPEAT 200 207 CXXCXGKG motif.

FT METAL 147 147 Zinc 1 (By similarity).

FT METAL 150 150 Zinc 1 (By similarity).

FT METAL 164 164 Zinc 2 (By similarity).

FT METAL 167 167 Zinc 2 (By similarity).

FT METAL 186 186 Zinc 2 (By similarity).

FT METAL 189 189 Zinc 2 (By similarity).
 FT METAL 200 200 Zinc 1 (By similarity).
 FT METAL 203 203 Zinc 1 (By similarity).
 SQ SEQUENCE 377 AA; 41027 MW; 37E9048F81A1A7A9 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 377;

Best Local Similarity 100.0%; Pred. No. 9.9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

DB 61 QKRAAYDQYGHAAFE 75

RESULT 7

ID DNAAJ_SALTY STANDARD; PRT; 378 AA.

AC Q60004;

DT 01-NOV-1997 (Rel. 35, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Chaperone protein dnaJ.

GN Name=dnaJ; OrderedLocuNames=STM0013, STY0013, t0013;

OS Salmonella typhimurium, and

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=602, 601;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=S.typhimurium; STRAIN=LT2;

RA Stephen R.J., Hinton J.C.D.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

RA McClelland M., Sanders K.E., Spieth J., Clifton S.W., Latreille P.,

RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;

RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2."
 RT Nature 413:852-856 (2001).
 RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=CT18;

RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;

RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,

RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

RA Krogh A., Larsen T.S., Leather S., Moule S., O'Goara P., Parry C.,

RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,

RA Whitehead S., Barrell B.G.;

RA "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18."
 RT Nature 413:848-852 (2001).
 RN [4]

RP SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=TY2 / ATCC 700931;

RX MEDLINE=22531367; PubMed=12644504;

RX DOI=10.1126/JB.185.7.2330-2337.2003;

RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;

RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18."
 RL J. Bacteriol. 185:2330-2337 (2003).
 CC -!- FUNCTION: Interacts with dnaK to disassemble a protein complex at
 CC the phage lambda origin of replication. Stimulates, jointly with
 CC grpE, the ATPase activity of dnaK.

```
CC -|- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- INDUCTION: By heat shock under the control of the htpR regulatory
CC protein (By similarity).
CC -|- SIMILARITY: Belongs to the dnaJ family.
CC -|- SIMILARITY: Contains 1 CR domain.
CC -|- SIMILARITY: Contains 1 J domain.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U58360; AAB02911.1; -.
DR EMBL; AB008693; AAL18977.1; -.
DR EMBL; AL627265; CAD01166.1; -.
DR EMBL; AB016834; AAO67747.1; -.
DR HSSP; P08622; 1EXX.
DR StyGene; SG10620; dnaJ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pdp.
DR InterPro; IPR003095; HspDnaJ.
DR InterPro; IPR011031; Multihem_cyt.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT INIT MET 0 0 By similarity.
FT DOMAIN 2 71 J-domain.
FT REPEAT 76 112 Gly-rich.
FT REPEAT 146 153 CXXCXGXG motif.
FT REPEAT 163 170 CXXCXGXG motif.
FT REPEAT 185 192 CXXCXGXG motif.
FT REPEAT 199 206 CXXCXGXG motif.
FT METAL 146 146 Zinc 1 (By similarity).
FT METAL 149 149 Zinc 1 (By similarity).
FT METAL 163 163 Zinc 2 (By similarity).
FT METAL 166 166 Zinc 2 (By similarity).
FT METAL 185 185 Zinc 2 (By similarity).
FT METAL 188 188 Zinc 2 (By similarity).
FT METAL 199 199 Zinc 1 (By similarity).
FT METAL 202 202 Zinc 1 (By similarity).
SQ SEQUENCE 378 AA; 41181 MW; 176EE64696F30A2 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 60 QKRAAYDQYGHAAFE 74

RESULT 8
Q8L3D3 PRELIMINARY; PRT; 379 AA.
AC Q8L3D3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 40.
```

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GN Name=dnaJ;
OS Colwellia maris (Vibrio sp. (strain ABE-11)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Colwelliaceae; Colwellia.
OX NCBI_TaxID=77524;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamauchi S., Okuyama H., Nishiyama Y., Hayashi H.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB084455; BAB91324.2; -.
DR HSSP; P08622; 1BQZ.
DR GO; GO:0051082; P:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pdp.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Heat shock.
SQ SEQUENCE 379 AA; 40995 MW; 58A2894D13F8E9FA CRC64;

Query Match 100.0%; Score 81; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 61 QKRAAYDQYGHAAFE 75

RESULT 9
Q66ES9 PRELIMINARY; PRT; 379 AA.
AC Q66ES9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Heat shock protein, DnaJ and GrpE stimulates ATPase activity of
DE DnaK.
GN Name=dnaJ; Synonyms=grpP, grpC; ORFNames=YPTB0612;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francoise V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the genome evolution of Yersinia pseudotuberculosis."
RT genome comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -|- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -|- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; BX936398; CAH19852.1; -.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
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DR PRINTS; PRO0625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGK; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
Metal-binding; Repeat; Zinc.
SQ SEQUENCE 379 AA; 41278 MW; AC1922FC3D707C93 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
   |||||
Db 61 QKRAAYDQYGHAAFE 75

RESULT 13
DnaJ_HAEIN
ID_DNAJ_HAEIN STANDARD; PRT; 382 AA.
AC P43735;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chapterone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=H11238;
OS Haemophilus influenzae;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D.; Adams M.D.; White O.; Clayton R.A.; Kirkness E.F.;
RA McKenney K.; Sutton G.G.; FitzHugh W.; Fields C.A.; Gocayne J.D.;
RA Scott J.D.; Shirley R.; Liu L.-I.; Glodek A.; Kelley J.M.;
RA Weidman J.F.; Phillips C.A.; Spriggs T.; Hedblom E.; Cotton M.D.;
RA Utterback T.R.; Hanna M.C.; Nguyen D.T.; Saudek D.M.; Brandon R.C.;
RA Fine L.D.; Fritchman J.L.; Fuhrmann J.L.; Geoghegan N.S.M.;
RA Gnehm C.L.; McDonald L.A.; Small K.V.; Fraser C.M.; Smith H.O.;
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
RT Science 269:496-512 (1995).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).
CC -!- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
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CC -----
CC EMBL; U32803; AAC22890.1; ALT_INIT.
CC HSP; P08622; 1BQ2.
CC TIGR; H11238; -.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGK.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR003095; Hsp DnaJ.
CC InterPro; IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ; 1.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGK; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGK; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
Metal-binding; Repeat; Zinc.
KW SEQUENCE 379 AA; 41212 MW; 3814B164D55F8CB9 CRC64;

DR PRINTS; PRO0625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGK; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
Metal-binding; Repeat; Zinc.
SQ SEQUENCE 379 AA; 41278 MW; AC1922FC3D707C93 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
   |||||
Db 61 QKRAAYDQYGHAAFE 75

RESULT 12
Q6D0B8 PRELIMINARY; PRT; 379 AA.
AC Q6D0B8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chapterone protein DnaJ.
GN Name=dnaJ; OrderedLocusNames=ECA3881;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S.; Sebaihia M.; Pritchard L.; Holden M.T.G.; Hyman L.J.;
RA Holeva M.C.; Thomson N.R.; Bentley S.D.; Churcher L.J.C.; Mungall K.;
RA Atkin R.; Bason N.; Brooks K.; Chillingworth T.; Clark K.; Doggett J.;
RA Fraser A.; Hance Z.; Hauser H.; Jagels K.; Moule S.; Norbertczak H.;
RA Ormond D.; Price C.; Quail M.A.; Sanders M.; Walker D.; Whitehead S.;
RA Salmond G.P.C.; Birch P.R.J.; Parkhill J.; Toth I.K.;
RA "Genome sequence of the enterobacterial phytopathogen Erwinia carotovora subsp. atroseptica and characterization of virulence factors.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).
CC -!- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC EMBL; BX950851; CAG76779.1; -.
CC GO; GO:0051082; F:unfolded protein binding; IEA.
CC GO; GO:006457; P:protein folding; IEA.
CC InterPro; IPR000345; CytC_heme_BS.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGK.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; HSP40_DnaJ_pap.
CC InterPro; IPR003095; Hsp DnaJ.
CC InterPro; IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ; 1.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGK; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGK; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
Metal-binding; Repeat; Zinc.
KW SEQUENCE 379 AA; 41212 MW; 3814B164D55F8CB9 CRC64;
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FT DOMAIN 3 72 J-domain.
 FT DOMAIN 77 110 Gly-rich.
 FT REPEAT 147 154 CXKXGKG motif.
 FT REPEAT 164 171 CXKXGKG motif.
 FT REPEAT 186 193 CXKXGKG motif.
 FT REPEAT 200 207 CXKXGKG motif.
 FT METAL 147 147 Zinc 1 (By similarity).
 FT METAL 150 150 Zinc 1 (By similarity).
 FT METAL 164 164 Zinc 2 (By similarity).
 FT METAL 167 167 Zinc 2 (By similarity).
 FT METAL 186 186 Zinc 2 (By similarity).
 FT METAL 189 189 Zinc 2 (By similarity).
 FT METAL 200 200 Zinc 1 (By similarity).
 FT METAL 203 203 Zinc 1 (By similarity).
 SQ SEQUENCE 382 AA; 41222 MW; 88508886FB2BC2B CRC64;

Query Match 100.0%; Score 81; DB 1; Length 382;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QKRAAYDQYGHAAFE 15
 |||||
 Db 61 QKRAAYDQYGHAAFE 75

RESULT 14

Q83MH4
 ID Q83MH4 PRELIMINARY; PRT; 386 AA.
 AC Q83MH4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Chapterone with DnaK; heat shock protein.
 GN Name=dnaJ; OrderedLocusNames=SP0015;
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=301 / Serotype 2a;
 RX MEDLINE=2272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC ENBL; AE015039; AAN41681.1; --
 DR HSP; P08622; 1EXK.
 DR GO; GO:0051082; P:unfolded protein binding; IEA.
 DR GO; GO:006260; P:DNA replication; IEA.
 DR GO; GO:006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXKXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR PRINTS; PF00684; DnaJ_CXKXGKG; 1.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.

DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00706; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXKXGKG; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 386 AA; 42279 MW; 172BC403A6E7D75E CRC64;

Query Match 100.0%; Score 81; DB 2; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QKRAAYDQYGHAAFE 15
 |||||
 Db 71 QKRAAYDQYGHAAFE 85

RESULT 15

DNAJ ACTAC
 ID DNAJ ACTAC STANDARD; PRT; 375 AA.
 AC P77856;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chapterone protein dnaJ.
 GN Name=dnaJ;
 OS Actinobacillus actinomycetemcomitans (Haemophilus
 actinomycetemcomitans).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Actinobacillus.
 OX NCBI_TaxID=714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y4;
 RX MEDLINE=98182595; PubMed=9522128;
 RA Yoshida A., Nakano Y., Yamashita Y., Yu H., Ohishi M., Koga T.;
 RT "Isolation and characterization of the dnaK operon from
 Actinobacillus actinomycetemcomitans.";
 RL DNA Seq. 8:93-98(1997).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- SIMILARITY: Contains 1 CR domain.
 CC -1- SIMILARITY: Contains 1 J domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC ENBL; D87753; BAA32697.1; --
 DR HSP; P08622; 1BQZ.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXKXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR InterPro; IPR011031; Multihaem_cyt.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXKXGKG; 1.
 DR PRINTS; PF00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00706; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXKXGKG; 1.
 KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
 FT DOMAIN 5 70 J-domain.
 FT DOMAIN 77 110 Gly-rich.

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FT REPEAT 145 152 CXXCXGXG motif.
FT REPEAT 162 169 CXXCXGXG motif.
FT REPEAT 184 191 CXXCXGXG motif.
FT REPEAT 198 205 CXXCXGXG motif.
FT METAL 145 145 Zinc 1 (By similarity).
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 162 162 Zinc 2 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
FT METAL 184 184 Zinc 2 (By similarity).
FT METAL 187 187 Zinc 2 (By similarity).
FT METAL 198 198 Zinc 1 (By similarity).
FT METAL 201 201 Zinc 1 (By similarity).
SQ SEQUENCE 375 AA; 41374 MW; CF9D286756FF44E1 CRC64;

Query Match 96.3%; Score 78; DB 1; Length 375;
Best Local Similarity 93.3%; Pred. No. 3.3e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 61 EKRAAYDQYGHAAFE 75

RESULT 16
Q6LUAG PRELIMINARY; PRT; 380 AA.
AC O6LUAG6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative DnaJ protein, DnaJ-class molecular chaperone with C-terminal
DE Zn finger domain.
GN Name=EC50015; OrderedLocusNames=PPRA0698;
OS Bacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; CR378665; CAG19119.1; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ; 1.
DR Pfam; PF00884; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ 1; 1.
DR PROSITE; PS50076; DnaJ 2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 380 AA; 40802 MW; 772DD9F069899B63 CRC64;

Query Match 96.3%; Score 78; DB 2; Length 380;
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Best Local Similarity 93.3%; Pred. No. 3.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 60 QKRAAYDQYGHAAFE 74

RESULT 17
DnaJ_VIBCH STANDARD; PRT; 381 AA.
AC O34242; O9KTP5;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=VC0856;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10942301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
RN SEQUENCE OF 1-80 FROM N.A.
RC STRAIN=Classical 569B / ATCC 25870 / Serotype O1;
RX MEDLINE=99150229; PubMed=10024539;
RA Chakrabarti S., Sengupta N., Chowdhury R.;
RT "Role of DnaK in vitro and in vivo expression of virulence factors
RT of Vibrio cholerae.";
RL Infect. Immun. 67:1025-1033(1999).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
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CC or send an email to license@isb-sib.ch).
DR EMBL; AE004171; AAF94018.1; -.
DR PIR; D82270; D82270.
DR HSP; P08622; 1BQZ.
DR TIGR; VC0856; -.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR011031; Multisubunit.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
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DR PRINTS; PR00625; DnaJ C.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 4 72
FT J-domain.
FT REPEAT 77 119
FT GLY-rich.
FT REPEAT 149 156
FT CXXCXGKG motif.
FT REPEAT 166 173
FT CXXCXGKG motif.
FT REPEAT 188 195
FT CXXCXGKG motif.
FT REPEAT 202 209
FT CXXCXGKG motif.
FT METAL 149 149
FT Zinc 1 (By similarity).
FT METAL 152 152
FT Zinc 1 (By similarity).
FT METAL 166 166
FT Zinc 2 (By similarity).
FT METAL 169 169
FT Zinc 2 (By similarity).
FT METAL 188 188
FT Zinc 2 (By similarity).
FT METAL 191 191
FT Zinc 1 (By similarity).
FT METAL 202 202
FT Zinc 1 (By similarity).
FT METAL 205 205
FT Zinc 1 (By similarity).
FT METAL 205 205
FT Zinc 1 (By similarity).
FT CONFLICT 37 38
FT NS -> TP (in Ref. 2).
FT CONFLICT 43 45
FT AAE -> CRG (in Ref. 2).
FT CONFLICT 49 51
FT EVK -> IQ (in Ref. 2).
FT CONFLICT 67 67
FT D -> E (in Ref. 2).
FT CONFLICT 71 71
FT H -> I (in Ref. 2).
FT CONFLICT 78 80
FT AGG -> RVV (in Ref. 2).
SQ SEQUENCE 381 AA; 40822 MW; 2188BE36D0315D5 CRC64;

Query Match 96.3%; Score 78; DB 1; Length 381;
Best Local Similarity 93.3%; Pred. No. 3.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75
||:|||||

RESULT 18

Q87RX2 PRELIMINARY; PRT; 381 AA.
ID Q87RX2
AC Q87RX2
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DnaJ protein.
GN OrderedLocusNames=VP0654;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RMD.2210633 / Serotype O3:K6;
RA MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC EMBL; AP005075; BAC58917.1; -.
DR HSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
Q8DF67 PRELIMINARY; PRT; 381 AA.
ID Q8DF67
AC Q8DF67
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DnaJ chaperone.
GN OrderedLocusNames=VW10354;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC EMBL; AS016798; AAC08881.1; -.
DR HSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR008971; HSP40_DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF0684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR008971; HSP40_DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF0684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.

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KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 381 AA; 41226 MW; 1F0783454AE538A6 CRC64;

Query Match          96.3%; Score 78; DB 2; Length 381;
Best Local Similarity 93.3%; Pred. No. 3.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 20
DNAJ_VIBHA
ID DNAJ_VIBHA STANDARD; PRT; 385 AA.
AC O87385;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ;
OS Vibrio harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98418481; PubMed=9747709; DOI=10.1007/s004380050803;
RA Klein G., Zmijewski M., Krzewska J., Czezakka M., Lipinska B.;
RT "Cloning and characterization of the dnaK heat shock operon of the
marine bacterium Vibrio harveyi."
RL Mol. Gen. Genet. 259:179-189(1998).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY639008; AAT39537.1; -.
DR HSSP; P08622; 1BQZ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR011031; Multihem_cyt.
DR Pfam; PF02226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT REPEAT 77 120 Gly-rich.
FT REPEAT 150 157 CXXCXGKG motif.
FT REPEAT 167 174 CXXCXGKG motif.
FT REPEAT 189 196 CXXCXGKG motif.
FT REPEAT 202 209 CXXCXGKG motif.
FT METAL 150 150 Zinc 1 (By similarity).

KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 381 AA; 41226 MW; 1F0783454AE538A6 CRC64;

Query Match          96.3%; Score 78; DB 2; Length 381;
Best Local Similarity 93.3%; Pred. No. 3.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 21
Q7MN84
ID Q7MN84 PRELIMINARY; PRT; 386 AA.
AC Q7MN84;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chaperone protein dnaJ.
GN OrderedLocusNames=V0833;
OS Vibrio vulnificus (strain VJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
pathogen."
RL Genome Res. 13:2577-2587(2003).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; AP005333; BAC93597.1; -.
DR HSSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006240; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 386 AA; 41786 MW; A774299EF281D6C0 CRC64;

Query Match          96.3%; Score 78; DB 2; Length 386;
Best Local Similarity 93.3%; Pred. No. 3.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QKRAAYDQYGHAAFE 15
 Db 66 QKRAAYDQYGHAAFE 80

RESULT 22

ID Q65U54 PRELIMINARY; PRT; 389 AA.
 AC Q65U54;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE DnaJ protein.
 GN Name=dnaJ; ORFNames=MS0899;
 OS Mannheimia succiniciproducens MBEL55E.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 OX NCBI_TaxID=221988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MBEL55E;
 RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
 RA Kim C.H., Jeong H., Hur C.-G., Kim J.G.;
 RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
 succiniciproducens.";
 RL Nat. Biotechnol. 0:0-0(2004).
 DR EMBL; AE016827; AAU37506.1; -.
 SQ SEQUENCE 389 AA; 42555 MW; 8DE1A0A8A47374B CRC64;

Query Match 96.3%; Score 78; DB 2; Length 389;
 Best Local Similarity 93.3%; Pred. No. 3.4e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
 Db 74 EKRAAYDQYGHAAFE 88

RESULT 23

ID DNAJ_RHILE STANDARD; PRT; 234 AA.
 AC Q3529;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chapterone protein dnaJ (Fragment).
 GN Name=dnaJ, leguminosarum.
 OS Rhizobium leguminosarum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OX NCBI_TaxID=384;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8401:PRLI;
 RA Simpkins S.A., Johnston A.W.B., James R.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- SIMILARITY: Contains 1 CR domain.
 CC -1- SIMILARITY: Contains 1 J domain.
 CC -----
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 CC -----
 CC EMBL; Y14649; CAA74983.1; -.

DR HSSP; P08622; 1BQZ.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM0271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
 FT DOMAIN 3 72 J-domain.
 FT DOMAIN 77 119 Gly-rich.
 FT REPEAT 149 156 CXXCXGKG motif.
 FT REPEAT 166 173 CXXCXGKG motif.
 FT REPEAT 188 195 CXXCXGKG motif.
 FT REPEAT 202 209 CXXCXGKG motif.
 FT METAL 149 149 Zinc 1 (By similarity).
 FT METAL 152 152 Zinc 1 (By similarity).
 FT METAL 166 166 Zinc 2 (By similarity).
 FT METAL 169 169 Zinc 2 (By similarity).
 FT METAL 188 188 Zinc 2 (By similarity).
 FT METAL 191 191 Zinc 2 (By similarity).
 FT METAL 202 202 Zinc 1 (By similarity).
 FT METAL 205 205 Zinc 1 (By similarity).
 FT NON_TER 234 234.
 SQ SEQUENCE 234 AA; 25268 MW; 2D8361F8495164E3 CRC64;

Query Match 95.1%; Score 77; DB 1; Length 234;
 Best Local Similarity 93.3%; Pred. No. 3.1e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
 Db 61 QKRAAYDQYGHAAFE 75

RESULT 24

Q93S23 PRELIMINARY; PRT; 331 AA.
 ID Q93S23;
 AC Q93S23;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DnaJ protein (Fragment).
 GN Name=dnaJ;
 OS Rhizobium tropici.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OX NCBI_TaxID=398;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CIAT899;
 RA Sanjuan J.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC EMBL; AJ311186; CAC38775.1; -.
 DR HSSP; P08622; 1BQZ.
 DR GO; GO:0051082; P:unfolded protein binding; IEA.
 DR GO; GO:0006260; P:DNA replication; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.

Gaps 0;

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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAPE 15
Db 61 OKRAAYDOYGHAAPE 75

RESULT 28
DNAJ_BUCAI
ID DNAJ_BUCAI STANDARD; PRT; 377 AA.
AC O32465;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chapterone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=PM0740;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.-J., Zhang Q., Li L.-L., Pautian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE006111; BAK02824.1; -.
CC HSP; P08622; 1BQZ.
CC InterPro: IPR002939; DnaJ_C.
CC InterPro: IPR001305; DnaJ_N.
CC InterPro: IPR001623; DnaJ_N.
CC InterPro: IPR008971; HSP40_DnaJ_pap.
CC InterPro: IPR003095; Hsp_DnaJ.
CC InterPro: IPR011031; Multihaem_cyt.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF01556; DnaJ_N; 1.
CC PRINTS; PS00684; DnaJ_CXXCXGXG; 1.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00637; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGXG; FALSE NEG.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.

Query Match 92.6%; Score 75; DB 1; Length 372;
Best Local Similarity 93.3%; Pred. No. 0.00011;

RESULT 27
DNAJ_PASMU
ID DNAJ_PASMU STANDARD; PRT; 372 AA.
AC Q9CNS2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 05-JUL-2004 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chapterone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=PM0740;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.-J., Zhang Q., Li L.-L., Pautian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
CC EMBL; AE006111; BAK02824.1; -.
CC HSP; P08622; 1BQZ.
CC InterPro: IPR002939; DnaJ_C.
CC InterPro: IPR001305; DnaJ_N.
CC InterPro: IPR001623; DnaJ_N.
CC InterPro: IPR008971; HSP40_DnaJ_pap.
CC InterPro: IPR003095; Hsp_DnaJ.
CC InterPro: IPR011031; Multihaem_cyt.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF01556; DnaJ_N; 1.
CC PRINTS; PS00684; DnaJ_CXXCXGXG; 1.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00637; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT REPEAT 143 150 Gly-rich.
FT REPEAT 160 167 CXXCXGXG motif.
FT REPEAT 182 189 CXXCXGXG motif.
FT REPEAT 196 203 CXXCXGXG motif.
FT METAL 143 143 Zinc 1 (By similarity).
FT METAL 146 146 Zinc 1 (By similarity).
FT METAL 160 160 Zinc 2 (By similarity).
FT METAL 163 163 Zinc 2 (By similarity).
FT METAL 182 182 Zinc 2 (By similarity).
FT METAL 185 185 Zinc 2 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 199 199 Zinc 1 (By similarity).
SQ SEQUENCE 372 AA; 40776 MW; 339B5FE137211D9A CRC64;

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FT DOMAIN 77 115 Gly-rich.
FT REPEAT 145 152 CXXCXGXG motif.
FT REPEAT 162 169 CXXCXGXG motif.
FT REPEAT 184 191 CXXCXGXG motif.
FT REPEAT 198 205 CXXCXGXG motif.
FT METAL 145 145 Zinc 1 (By similarity).
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 162 162 Zinc 2 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
FT METAL 184 184 Zinc 2 (By similarity).
FT METAL 187 187 Zinc 2 (By similarity).
FT METAL 198 198 Zinc 1 (By similarity).
FT METAL 201 201 Zinc 1 (By similarity).
FT CONFLICT 185 185 P -> S (in Ref. 1).
FT CONFLICT 270 270 I -> K (in Ref. 1).
SQ SEQUENCE 377 AA; 42344 MW; F232B95530CC298B CRC64;

Query Match 92.6%; Score 75; DB 1; Length 377;
Best Local Similarity 86.7%; Pred. No. 0.00011;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
Db :||:|||||||

RESULT 29
DNAJ BUCAP STANDARD; PRT; 378 AA.
ID DNAJ BUCAP STANDARD; PRT; 378 AA.
AC Q8K979;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocNames=BUSg145;
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438; DOI=10.1126/science.1071278;
RA Tamás I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
RA "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
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CC -----
CC EMBL; AE014090; AAM67713.1; -.
CC HSP; P08622; 1BQZ.
CC InterPro; IPR002939; DnaJ C.
CC InterPro; IPR001305; DnaJ_CXXCXGXG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; HSP40_DnaJ_pap.
CC InterPro; IPR003095; Hsp_DnaJ.
CC InterPro; IPR011031; Multihem_cyt.
CC Pfam; PF00226; DnaJ; 1.
CC Pfam; PF01556; DnaJ_C; 1.

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DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; FALSE NEG.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT REPEAT 77 116 Gly-rich.
FT REPEAT 146 153 CXXCXGXG motif.
FT REPEAT 163 170 CXXCXGXG motif.
FT REPEAT 185 192 CXXCXGXG motif.
FT REPEAT 199 206 CXXCXGXG motif.
FT METAL 146 146 Zinc 1 (By similarity).
FT METAL 149 149 Zinc 1 (By similarity).
FT METAL 163 163 Zinc 2 (By similarity).
FT METAL 166 166 Zinc 2 (By similarity).
FT METAL 185 185 Zinc 2 (By similarity).
FT METAL 188 188 Zinc 2 (By similarity).
FT METAL 199 199 Zinc 1 (By similarity).
FT METAL 202 202 Zinc 1 (By similarity).
SQ SEQUENCE 378 AA; 42469 MW; BB73F48DAF7A2D34 CRC64;

Query Match 91.4%; Score 74; DB 1; Length 378;
Best Local Similarity 86.7%; Pred. No. 0.00017;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
Db :||:|||||||

RESULT 30
DNAJ NEIMA STANDARD; PRT; 373 AA.
ID DNAJ NEIMA STANDARD; PRT; 373 AA.
AC P63968; P57107;
DT 16-OCT-2001 (Rel. 40, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocNames=NMA0209;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Chillingworth T.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RA "Complete DNA sequence of a serogroup A strain of Neisseria
RA meningitidis Z2491.";
RL Nature 404:502-506(2000).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COPACITOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC
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CC -----

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-----
CC EMBL; AL162752; CAB83522.1; -.
CC HSSP; P08622; 1BQZ.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; Hsp40_DnaJ_pap.
CC InterPro; IPR003095; Hsp_DnaJ.
CC InterPro; IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT REPEAT 147 154 Gly-rich.
FT REPEAT 164 171 CXXCXGKG motif.
FT REPEAT 186 193 CXXCXGKG motif.
FT REPEAT 200 207 CXXCXGKG motif.
FT METAL 147 147 Zinc 1 (By similarity).
FT METAL 150 150 Zinc 1 (By similarity).
FT METAL 164 164 Zinc 2 (By similarity).
FT METAL 167 167 Zinc 2 (By similarity).
FT METAL 186 186 Zinc 2 (By similarity).
FT METAL 189 189 Zinc 2 (By similarity).
FT METAL 200 200 Zinc 1 (By similarity).
FT METAL 203 203 Zinc 1 (By similarity).
SQ SEQUENCE 373 AA; 40585 MW; 4D881E20A5D831CF CRC64;

Query Match 90.1%; Score 73; DB 1; Length 373;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 EKRAAYDQYGHAAFE 75

RESULT 31
DnaJ_NEIMB
ID DnaJ_NEIMB STANDARD; PRT; 373 AA.
AC P63969; P57107;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocustNames=NMB0059;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hackey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Citterio H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
```

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Science 287:1809-1815(2000).
-!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).
-!- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the dnaJ family.
-!- SIMILARITY: Contains 1 CR domain.
-!- SIMILARITY: Contains 1 J domain.
-----
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or send an email to license@isb-sib.ch).
-----
CC EMBL; AS003365; AAP40528.1; -.
CC PIR; D81242; D81242.
CC HSSP; P08622; 1BQZ.
CC TIGR; NMB0059; -.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; Hsp40_DnaJ_pap.
CC InterPro; IPR003095; Hsp_DnaJ.
CC InterPro; IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT REPEAT 147 154 Gly-rich.
FT REPEAT 164 171 CXXCXGKG motif.
FT REPEAT 186 193 CXXCXGKG motif.
FT REPEAT 200 207 CXXCXGKG motif.
FT METAL 147 147 Zinc 1 (By similarity).
FT METAL 150 150 Zinc 1 (By similarity).
FT METAL 164 164 Zinc 2 (By similarity).
FT METAL 167 167 Zinc 2 (By similarity).
FT METAL 186 186 Zinc 2 (By similarity).
FT METAL 189 189 Zinc 2 (By similarity).
FT METAL 200 200 Zinc 1 (By similarity).
FT METAL 203 203 Zinc 1 (By similarity).
SQ SEQUENCE 373 AA; 40585 MW; 4D881E20A5D831CF CRC64;

Query Match 90.1%; Score 73; DB 1; Length 373;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 EKRAAYDQYGHAAFE 75

RESULT 32
DnaJ_BRUOV
ID DnaJ_BRUOV STANDARD; PRT; 375 AA.
AC Q05980;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
DE Name=dnaJ;
OS Brucella ovis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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OC Brucellaceae; Brucella.
OX NCBI_TaxID=236;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25840 / 63/290T;
RX MEDLINE=93094135; PubMed=1459952;
RA Cellier M.F.M., Teyssier J., Nicolas M., Liautard J.P., Marti J.,
RT "Cloning and characterization of the Brucella ovis heat shock protein
RT DnaK functionally expressed in Escherichia coli.";
RL J. Bacteriol. 174:8036-8042(1992).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: By heat shock.
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M95799; AAC36133.1; -.
DR PIR; B47042; B47042.
DR HSP; P08622; 1BQZ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_p.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multicnaem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; P00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
DR Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT DOMAIN 4 69 J-domain.
FT DOMAIN 77 106 Gly-rich.
FT REPEAT 146 133 CXXCXGXG motif.
FT REPEAT 163 170 CXXCXGXG motif.
FT REPEAT 185 192 CXXCXGXG motif.
FT REPEAT 199 206 CXXCXGXG motif.
FT METAL 146 146 Zinc 1 (By similarity).
FT METAL 149 149 Zinc 1 (By similarity).
FT METAL 163 163 Zinc 2 (By similarity).
FT METAL 166 166 Zinc 2 (By similarity).
FT METAL 185 185 Zinc 2 (By similarity).
FT METAL 188 188 Zinc 2 (By similarity).
FT METAL 199 199 Zinc 1 (By similarity).
FT METAL 202 202 Zinc 1 (By similarity).
SQ SEQUENCE 375 AA; 41021 MW; 61CB5F9FA2DC73D CRC64;

Query Match 90.1%; Score 73; DB 1; Length 375;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDOYGHAAFE 15
Db |||||||:|||||
60 QKRAAYDRFGHAAFE 74

RESULT 33
Q98DD2

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ID Q98DD2 PRELIMINARY; PRT; 376 AA.
AC Q98DD2;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein; DnaJ.
GN OrderedLocuNames=ml14755;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsuoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AP003004; BAB51339.1; -.
DR HSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006250; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_p.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; P00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 376 AA; 41201 MW; AFA2EAB4C2186E7 CRC64;

Query Match 90.1%; Score 73; DB 2; Length 376;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDOYGHAAFE 15
Db |||||||:|||||
60 QKRAAYDRFGHAAFE 74

RESULT 34
DnaJ_AGR75
ID DnaJ_AGR75 STANDARD; PRT; 377 AA.
AC P50018;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocuNames=Atu0121, AGR_C_192;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

```



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OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Sebubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Neeter E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RL C58."
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houniel K., Gordon J., Vaubin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328 (2001).
RN [3]
RP SEQUENCE OF 1-66 FROM N.A.
RX MEDLINE=96011387; PubMed=7592349;
RA Segal G., Ron E.Z.;
RT "The dnaJ operon of Agrobacterium tumefaciens: transcriptional
RT analysis and evidence for a new heat shock promoter."
RL J. Bacteriol. 177:5952-5958 (1995).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- INDUCTION: By heat shock.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
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CC -----
DR EMBL; AE008986; AAU41146.1; -.
DR EMBL; AE007953; AX85941.1; -.
DR EMBL; X87113; CAA60593.1; -.
DR PIR; AD2591; AD2591.
DR PIR; D97373; D97373.
DR PIR; I39586; I39586.
DR HSSP; P08622; 1BQZ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; MultThaen_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT DOMAIN 77 109 Gly-rich.
FT REPEAT 151 158 CXXCXGKG motif.
FT REPEAT 168 175 CXXCXGKG motif.
FT REPEAT 190 197 CXXCXGKG motif.
FT REPEAT 204 211 CXXCXGKG motif.
FT METAL 151 151 Zinc 1 (By similarity).
FT METAL 154 154 Zinc 1 (By similarity).
FT METAL 168 168 Zinc 2 (By similarity).
FT METAL 171 171 Zinc 2 (By similarity).
FT METAL 190 190 Zinc 2 (By similarity).
FT METAL 193 193 Zinc 2 (By similarity).
FT METAL 204 204 Zinc 1 (By similarity).
FT METAL 207 207 Zinc 1 (By similarity).
FT CONFLICT 4 A -> R (in Ref. 3).
SQ SEQUENCE 377 AA; 40894 MW; 0E68A1D30754D18A CRC64;
Query Match 90.1%; Score 73; DB 1; Length 377;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKEAAAYDQYGHAAFE 15
| | | | | : | | | |
DB 61 QKEAAAYDRFGHAAFE 75
RESULT 35
DNAJ BRUME
ID DNAJ BRUME STANDARD; PRT; 377 AA.
AC Q8VE77;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
OS Name=dnaJ; OrderedLocustNames=BMEI2001;
GN Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=294559;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=16M / ATCC 23456 / Biotype 1;
RX PubMed=11756688; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Muejer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE009632; AAL53182.1; -.
DR PIR; AC3502; AC3502.
DR HSSP; P08622; 1BQZ.
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DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR PROSITE; PS00076; DnaJ_1; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 4 69 J-domain.
FT REPEAT 77 106 Gly-rich.
FT REPEAT 148 155 CXXCXGKG motif.
FT REPEAT 165 172 CXXCXGKG motif.
FT REPEAT 187 194 CXXCXGKG motif.
FT REPEAT 201 208 CXXCXGKG motif.
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 151 151 Zinc 1 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
FT METAL 168 168 Zinc 2 (By similarity).
FT METAL 187 187 Zinc 2 (By similarity).
FT METAL 190 190 Zinc 2 (By similarity).
FT METAL 201 201 Zinc 1 (By similarity).
FT METAL 204 204 Zinc 1 (By similarity).
SQ SEQUENCE 377 AA; 41078 MW; E66AA1F16606E775 CRC64;

Query Match 90.1%; Score 73; DB 1; Length 377;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 60 QKRAAYDFGHAAFE 74

RESULT 36
ID DnaJ BRUSU STANDARD; PRT; 377 AA.
AC Q8FXL1,
DT 29-MAR-2004 (Rel. 43, Created)
DT 25-OCT-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chapterone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=BR2126;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=2247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.B., Hoover D.B., Lindler L.E., Halling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.

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-----
EMBL; AE014500; AAN31016.1; -.
DR PIR; AC3502; AC3502.
DR HSSP; P08622; LBQZ.
DR TIGR; BR2126; -.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 4 69 J-domain.
FT REPEAT 77 106 Gly-rich.
FT REPEAT 148 155 CXXCXGKG motif.
FT REPEAT 165 172 CXXCXGKG motif.
FT REPEAT 187 194 CXXCXGKG motif.
FT REPEAT 201 208 CXXCXGKG motif.
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 151 151 Zinc 1 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
FT METAL 168 168 Zinc 2 (By similarity).
FT METAL 187 187 Zinc 2 (By similarity).
FT METAL 190 190 Zinc 2 (By similarity).
FT METAL 201 201 Zinc 1 (By similarity).
FT METAL 204 204 Zinc 1 (By similarity).
SQ SEQUENCE 377 AA; 41078 MW; E66AA1F16606E775 CRC64;

Query Match 90.1%; Score 73; DB 1; Length 377;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 60 QKRAAYDFGHAAFE 74

RESULT 37
Q6RSNS PRELIMINARY; PRT; 379 AA.
AC Q6RSNS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DnaJ.
GN Name=dnaJ;
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RUOR.
RA Hennessy F., Boshoff A., Blatch G.L.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
```

DR InterPro: IPR005829; Sug_transporter.
DR Pfam: PF00226; DnaJ_1.
DR Pfam: PF01556; DnaJ_C_1.
DR Pfam: PF00684; DnaJ_CXXCXGK; 1.
DR PRINTS: PR00625; DnaJPROTEIN.
DR SMART: SM00271; DnaJ_1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS00636; DnaJ_1; 1.
DR PROSITE: PS0076; DnaJ_2; 1.
DR PROSITE: PS00637; DnaJ_CXXCXGK; 1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
KW Chaperone; Complete proteome; DNA_replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 380 AA; 42171 MW; 5B222DB2C5FE0BA8 CRC64;

Query Match 90.1%; Score 73; DB 2; Length 380;
Blast Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
| | | | | : | | | | |
Db 60 QKRAAYDRFGHAAFE 74

RESULT 39

Q6G553 PRELIMINARY; PRT; 381 AA.

ID Q6G553 AC Q6G553;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein DnaJ.
DS Name_dnaJ1; OrderedLocusNames=BH00660;
GN Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=38323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49882 / Houston 1;
RC PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scola B., Holmberg M., Andersson S.G.E.;
RT "The louise-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
DR EMBL: BX897699; CAP26882.1; -;
DR GO: GO:0051082; F:unfolded protein binding; IEA.
DR GO: GO:0006260; F:DNA replication; IEA.
DR GO: GO:0006457; P:protein folding; IEA.
DR GO: GO:0006986; P:response to unfolded protein; IEA.
DR InterPro: IPR000345; CytC_heme_BS.
DR InterPro: IPR02939; DnaJ_C.
DR InterPro: IPR001305; DnaJ_CXXCXGK.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR008971; HSP40_DnaJ_pep.
DR InterPro: IPR003095; Hsp DnaJ.
DR InterPro: IPR005829; Sug_transporter.
DR Pfam: PF00226; DnaJ_1.
DR Pfam: PF01556; DnaJ_C_1.
DR Pfam: PF00684; DnaJ_CXXCXGK; 1.
DR PRINTS: PR00625; DnaJPROTEIN.
DR SMART: SM00271; DnaJ_1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS00636; DnaJ_1; 1.
DR PROSITE: PS0076; DnaJ_2; 1.
DR PROSITE: PS00637; DnaJ_CXXCXGK; 1.

```
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 381 AA; 42248 MW; 738B5B7C9BD6C111 CRC64;

Query Match 90.1%; Score 73; DB 2; Length 381;
Best Local Similarity 86.7%; Pred. No. 0.00026;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
   |||||:|||||
Db 60 QKRAAYDRGHAAFE 74

RESULT 40
DNAME RHOPA
ID DNAME RHOPA STANDARD; PRT; 379 AA.
AC O6NCY3.
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocustNames=RPA0334;
OS Rhodopseudomonas palustris
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.B., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris."
RL Nat. Biotechnol. 22:55-61(2004).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; BX572594; CAE25778.1; -.
DR PROSITE; PS00636; DNAME 1; 1.
DR PROSITE; PS00637; DNAME CXXCXGKG; 1.
DR Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 7 72 J-domain.
FT DOMAIN 79 118 Gly-rich.
FT REPEAT 148 155 CXXCXGKG motif.
FT REPEAT 165 172 CXXCXGKG motif.
FT REPEAT 187 194 CXXCXGKG motif.
FT REPEAT 201 208 CXXCXGKG motif.
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 151 151 Zinc 1 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
FT METAL 168 168 Zinc 2 (By similarity).
FT METAL 187 187 Zinc 2 (By similarity).
FT METAL 190 190 Zinc 2 (By similarity).
FT METAL 201 201 Zinc 1 (By similarity).

FT METAL 204 204 Zinc 1 (By similarity).
SQ SEQUENCE 379 AA; 40992 MW; 53048356B1617B10 CRC64;

Query Match 88.9%; Score 72; DB 1; Length 379;
Best Local Similarity 92.9%; Pred. No. 0.00036;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
   |||||:|||||
Db 64 KRAAYDRYGHAAFE 77

RESULT 41
DNAME RHOS7
ID DNAME RHOS7 STANDARD; PRT; 379 AA.
AC O08356;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ;
OS Rhodopseudomonas sp. (strain No.7).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=269092;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97214635; PubMed=9061015; DOI=10.1016/S0167-4781(96)00222-9;
RA Momma K., Inui M., Yamagata H., Yukawa H.;
RT "Cloning of dnaK and dnaJ homologous genes from a purple non-sulfur
RT bacterium Rhodopseudomonas species."
RL Biochim. Biophys. Acta 1350:235-239(1997).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D78133; BAA19797.1; -.
DR HSP; P08622; LBQZ.
DR InterPro; IPR002939; DNAME C.
DR InterPro; IPR001305; DNAME CXXCXGKG.
DR InterPro; IPR001623; DNAME N.
DR InterPro; IPR003095; Hsp DNAME.
DR InterPro; IPR011031; Multihem_cyt.
DR Pfam; PF00226; DNAME 1.
DR Pfam; PF01556; DNAME C; 1.
DR Pfam; PF00684; DNAME CXXCXGKG; 1.
DR PRINTS; PR00625; DNAME PROTEIN.
DR SMART; SM00271; DNAME 1.
DR PROSITE; PS00636; DNAME 1; 1.
DR PROSITE; PS00076; DNAME 2; 1.
DR PROSITE; PS00637; DNAME CXXCXGKG; 1.
DR Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT DOMAIN 7 72 J-domain.
FT DOMAIN 79 118 Gly-rich.
FT REPEAT 148 155 CXXCXGKG motif.
FT REPEAT 165 172 CXXCXGKG motif.
FT REPEAT 187 194 CXXCXGKG motif.
FT REPEAT 201 208 CXXCXGKG motif.
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 151 151 Zinc 1 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
```

FT METAL 168 168 Zinc 2 (By similarity).
 FT METAL 187 187 Zinc 2 (By similarity).
 FT METAL 190 190 Zinc 2 (By similarity).
 FT METAL 201 201 Zinc 1 (By similarity).
 FT METAL 204 204 Zinc 1 (By similarity).
 SQ SEQUENCE 379 AA; 40392 MW; 53049356B1617B10 CRC64;

Query Match 88.9%; Score 72; DB 1; Length 379;
 Best Local Similarity 92.9%; Pred. No. 0.00038;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
 |||||:|||||
 Db 64 KRAAYDQYGHAAFE 77

RESULT 42
 Q8RB67 PRELIMINARY; PRT; 384 AA.
 AC Q8RB67;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Molecular chaperones (Contain C-terminal Zn finger domain).
 GN Name=DnaJ; OrderedLocNames=TrE0956;
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.
 NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4;
 RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of the T. tengcongensis genome.";
 RL Genome Res. 12:689-700(2002).
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
 the ATPase activity of dnaK (By similarity).
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the dnaJ family.
 DR EMBL; AE013061; AM24212.1; -.
 DR HSP; P08622; 1BQZ.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR001305; DnaJ_CXKXGKXG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR PRINTS; PR00684; DnaJ_CXKXGKXG; 1.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00636; DnaJ_2; 1.
 DR PROSITE; PS00776; DnaJ_1; 1.
 DR Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 384 AA; 42718 MW; 92B39791273F4094 CRC64;

Query Match 88.9%; Score 72; DB 2; Length 384;
 Best Local Similarity 86.7%; Pred. No. 0.00039;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
 |||||:|||||
 Db 61 QKRAAYDQYGHAAFE 75

RESULT 43
 Q7VQL3 PRELIMINARY; PRT; 377 AA.
 AC Q7VQL3;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DnaJ protein.
 GN Name=dnaJ; OrderedLocNames=Bf1115;
 OS Candidatus Blochmannia floridanus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
 NCBI_TaxID=203907;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22784745; PubMed=12886019; DOI=10.1073/pnas.1533499100;
 RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
 Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B.,
 van Ham R.C.H.J., Gross R., Moya A.;
 RT "The genome sequence of Blochmannia floridanus: comparative analysis
 of reduced genomes";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).
 DR ENBL; BX248584; CAD83636.1; -.
 DR HSP; P08622; 1BQZ.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXKXGKXG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR PRINTS; PR00684; DnaJ_CXKXGKXG; 1.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00776; DnaJ_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 377 AA; 41379 MW; 2047D0E868DB2A9E CRC64;

Query Match 86.4%; Score 70; DB 2; Length 377;
 Best Local Similarity 80.0%; Pred. No. 0.00085;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
 :|||:|||||
 Db 61 EKRSAYDQYGHAAFE 75

RESULT 44
 DNAJ_PASHA STANDARD; PRT; 379 AA.
 ID DNAJ_PASHA
 AC 052065;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chaperone protein dnaJ.
 GN Name=dnaJ;
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Serotype A1;
 RA Al S.L., Lo R.Y.C.;
 RT "The dnaK and dnaJ chaperone genes of Pasteurella haemolytica A1";
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
 the ATPase activity of dnaK (By similarity).
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the dnaJ family.
 CC -!- SIMILARITY: Contains 1 CR domain.
 CC -!- SIMILARITY: Contains 1 J domain.
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 CC -----

CC EMBL; AF017730; AAB94555.1; -.
 DR HSSP; P08622; 1BQZ.
 DR InterPro; IPR002939; DnaJ C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp DnaJ.
 DR InterPro; IPR011031; Multihaem_cyt.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 DR Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
 FT DOMAIN 5 70 J-domain.
 FT DOMAIN 77 119 Gly-rich.
 FT REPEAT 149 156 CXXCXGKG motif.
 FT REPEAT 166 173 CXXCXGKG motif.
 FT REPEAT 188 195 CXXCXGKG motif.
 FT REPEAT 202 209 CXXCXGKG motif.
 FT METAL 149 149 Zinc 1 (By similarity).
 FT METAL 152 152 Zinc 1 (By similarity).
 FT METAL 166 166 Zinc 2 (By similarity).
 FT METAL 169 169 Zinc 2 (By similarity).
 FT METAL 188 188 Zinc 2 (By similarity).
 FT METAL 191 191 Zinc 2 (By similarity).
 FT METAL 202 202 Zinc 1 (By similarity).
 FT METAL 205 205 Zinc 1 (By similarity).
 SQ SEQUENCE 379 AA; 41185 MW; 5467F5546219A98D CRC64;

Query Match 86.4%; Score 70; DB 1; Length 379;
 Best Local Similarity 80.0%; Pred. No. 0.00085;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 :|||:|||||:
 Db 61 EKXAMYDQYGHAAFE 75

RESULT 45
 DnaJ_BUCBP STANDARD; PRT; 383 AA.
 ID DnaJ_BUCBP
 AC Q89AU7;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Chaperone protein dnaJ.
 GN Name=dnaJ; OrderedLocustNames=bbp141;
 OS Buchnera aphidicola (subsp. Baizongia pistaciae).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=135842;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=1252265; DOI=10.1073/pnas.0235981100;
 RA van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
 RA Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

RA Tanames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
 RT "Reductive genome evolution in Buchnera aphidicola.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -!- COPACIT: Binds 2 zinc ions per monomer (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the dnaJ family.
 CC -!- SIMILARITY: Contains 1 CR domain.
 CC -!- SIMILARITY: Contains 1 J domain.
 CC -----

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 CC -----

CC EMBL; AE014016; AAO26875.1; -.
 DR HSSP; P08622; 1BQZ.
 DR InterPro; IPR002939; DnaJ C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp DnaJ.
 DR InterPro; IPR011031; Multihaem_cyt.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; FALSE NEG.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 FT DOMAIN 5 70 J-domain.
 FT DOMAIN 77 120 Gly-rich.
 FT REPEAT 150 157 CXXCXGKG motif.
 FT REPEAT 167 174 CXXCXGKG motif.
 FT REPEAT 189 196 CXXCXGKG motif.
 FT REPEAT 203 210 CXXCXGKG motif.
 FT METAL 150 150 Zinc 1 (By similarity).
 FT METAL 153 153 Zinc 1 (By similarity).
 FT METAL 167 167 Zinc 2 (By similarity).
 FT METAL 170 170 Zinc 2 (By similarity).
 FT METAL 189 189 Zinc 2 (By similarity).
 FT METAL 192 192 Zinc 2 (By similarity).
 FT METAL 203 203 Zinc 1 (By similarity).
 FT METAL 206 206 Zinc 1 (By similarity).
 SQ SEQUENCE 383 AA; 43299 MW; 881F48797684838D CRC64;

Query Match 86.4%; Score 70; DB 1; Length 383;
 Best Local Similarity 80.0%; Pred. No. 0.00086;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 :|||:|||||:
 Db 61 KKRTAYDQYGHAAFE 75

RESULT 46
 Q8KYX6 PRELIMINARY; PRT; 382 AA.
 ID Q8KYX6
 AC Q8KYX6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DnaJ protein.
 GN Name=dnaJ;
 OS uncultured proteobacterium.
 OC Bacteria; Proteobacteria; environmental samples.

```

OX NCBI_TaxID=153809;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Frazer C.M., DeLong E.F.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633 (2002).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AB008921; AAM48697.1; -.
DR HSSP; P08622; 1BQZ.
DR GO; GO:0051082; P:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR00345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR EMBL; U57637; AAC45474.1; -.
DR HSSP; P08622; 1XBL.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJ_PROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
SQ SEQUENCE 382 AA; 40509 MW; 8852P4CEIDCT5F5F CRC64;

Query Match 85.2%; Score 69; DB 2; Length 382;
Best Local Similarity 85.7%; Pred. No. 0.0013;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db :||||:|||||
62 KRAAYDRYGHAAFE 75

RESULT 47
DNAJ_RHOCA STANDARD; PRT; 384 AA.
AC Q52702;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ;
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33303 / B10;
RA Nickel C.M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U57637; AAC45474.1; -.
DR HSSP; P08622; 1XBL.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJ_PROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
SQ SEQUENCE 384 AA; 40692 MW; 607E94189807470B CRC64;

Query Match 85.2%; Score 69; DB 1; Length 384;
Best Local Similarity 85.7%; Pred. No. 0.0013;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db :||||:|||||
62 KRAAYDRYGHAAFE 75

RESULT 48
DNAJ_EYRHH STANDARD; PRT; 370 AA.
AC Q05626;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ;
OS Erysipelothrix rhusiopathiae.
OC Bacteria; Firmicutes; Mollicutes; Anaeroplasmatales;
OC Erysipelotrichaceae; Erysipelothrix.
OX NCBI_TaxID=1648;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B1-6P;
RX MEDLINE=93366167; PubMed=8359682; DOI=10.1016/0378-1097(93)90186-6;
RA Rockabrand D., Partridge J., Kraska J., Blum P.;
RT "Nucleotide sequence analysis and heterologous expression of the
RT Erysipelothrix rhusiopathiae dnaJ gene.";
RL FEMS Microbiol. Lett. 111:79-85(1993).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

```

CC -1- INDUCTION: By heat shock.
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- SIMILARITY: Contains 1 CR domain.
 CC -1- SIMILARITY: Contains 1 J domain.
 CC -----
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 CC -----

DR EMBL; L081110; AAA71922.1; -.
 DR HSSP; P08622; 1BQZ.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR InterPro; IPR011031; Multihaem_cyt.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
 FT DOMAIN 4 72 J-domain.
 FT REPEAT 77 106 Gly-rich.
 FT REPEAT 147 154 CXXCXGKG motif.
 FT REPEAT 164 171 CXXCXGKG motif.
 FT REPEAT 190 197 CXXCXGKG motif.
 FT REPEAT 204 211 CXXCXGKG motif.
 FT METAL 147 147 Zinc 1 (By similarity).
 FT METAL 150 150 Zinc 1 (By similarity).
 FT METAL 164 164 Zinc 2 (By similarity).
 FT METAL 167 167 Zinc 2 (By similarity).
 FT METAL 190 190 Zinc 2 (By similarity).
 FT METAL 193 193 Zinc 2 (By similarity).
 FT METAL 204 204 Zinc 1 (By similarity).
 FT METAL 207 207 Zinc 1 (By similarity).
 SQ SEQUENCE 370 AA; 40331 MW; 9A2B0F0E4546767D CRC64;

Query Match 84.0%; Score 68; DB 1; Length 370;
 Best Local Similarity 80.0%; Pred. No. 0.0019;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
 |||||:||||:
 Db 61 QKRAAYDQYGHAAFD 75

RESULT 49
 ID DnaJ_BRAJA STANDARD; PRT; 377 AA.
 AC P943I9;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chapterone protein dnaJ.
 GN Names=dnaJ; OrderedLocusNames=blr0680;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110spc4;
 RX MEDLINE=97261868; PubMed=9108282; DOI=10.1007/s004380050408;
 RA Minder A.C., Narberhaus F., Babet M., Hennecke H., Fischer H.-M.;

RT "The dnaJ operon belongs to the sigma32-dependent class of heat shock
 RL genes in Bradyrhizobium japonicum.";
 RN Mol. Gen. Genet. 254:195-206(1997).
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RX MEDLINE=22484988; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RL Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- SIMILARITY: Contains 1 CR domain.
 CC -1- SIMILARITY: Contains 1 J domain.
 CC -----
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 CC -----

DR EMBL; Y09633; CAA70848.1; -.
 DR EMBL; AP005937; BAC45945.1; -.
 DR HSSP; P08622; 1BQZ.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR InterPro; IPR011031; Multihaem_cyt.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Chapterone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 FT DOMAIN 8 73 J-domain.
 FT REPEAT 79 118 Gly-rich.
 FT REPEAT 148 155 CXXCXGKG motif.
 FT REPEAT 165 172 CXXCXGKG motif.
 FT REPEAT 187 194 CXXCXGKG motif.
 FT REPEAT 201 208 CXXCXGKG motif.
 FT METAL 148 148 Zinc 1 (By similarity).
 FT METAL 151 151 Zinc 1 (By similarity).
 FT METAL 165 165 Zinc 2 (By similarity).
 FT METAL 168 168 Zinc 2 (By similarity).
 FT METAL 187 187 Zinc 2 (By similarity).
 FT METAL 190 190 Zinc 2 (By similarity).
 FT METAL 201 201 Zinc 1 (By similarity).
 FT METAL 204 204 Zinc 1 (By similarity).
 SQ SEQUENCE 377 AA; 40945 MW; 7FE38A8EBC9B1BAA CRC64;

Query Match 84.0%; Score 68; DB 1; Length 377;
 Best Local Similarity 85.7%; Pred. No. 0.0019;
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
 |||||:||||:
 Db 65 KRAAYDQYGHAAFE 78

RESULT 50

DNAJ_METSS STANDARD; PRT; 371 AA.

AC Q92PFC5; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 05-JUL-2004 (Rel. 44, Last annotation update)

DE Chaperone protein DnaJ.

GN Name=dnaJ; (strain SS1 / DSM 11726).

OS Methylovorus sp. (strain SS1 / DSM 11726).

OC Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales;

OC Methylophilaceae; Methylovorus.

OX NCBI_TaxID=81683;

RN [1]

RP SEQUENCE FROM N.A.

RA Eom C.Y., Kim Y.M.;

RT "grpE, dnaK, and dnaJ genes of Methylovorus sp. strain SS1 DSM11726.";

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,

CC the ATPase activity of dnaK (by similarity).

CC -!- COPACITOR: Binds 2 zinc ions per monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the dnaJ family.

CC -!- SIMILARITY: Contains 1 CR domain.

CC -!- SIMILARITY: Contains 1 J domain.

CC -----

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CC -----

EMBL; AF106835; AAC95379.1; -.

HSSP; P08622; 1BQZ.

InterPro; IPR002939; DnaJ_C.

InterPro; IPR001305; DnaJ_CXXCXGKG.

InterPro; IPR001623; DnaJ_N.

InterPro; IPR003095; Hsp_DnaJ.

InterPro; IPR011031; Multithaem_cyt.

Pfam; PF00226; DnaJ_1.

Pfam; PF01556; DnaJ_C; 1.

Pfam; PF00684; DnaJ_CXXCXGKG; 1.

PRINTS; PR00625; DnaJPROTEIN.

SMART; SM00271; DnaJ_1.

PROSITE; PS00636; DnaJ_1; 1.

PROSITE; PS00076; DnaJ_2; 1.

PROSITE; PS00637; DnaJ_CXXCXGKG; 1.

KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.

FT DOMAIN 5 70

FT DOMAIN 79 115

FT REPEAT 145 152

FT REPEAT 162 169

FT REPEAT 184 191

FT REPEAT 198 205

FT METAL 145 145

FT METAL 148 148

FT METAL 162 162

FT METAL 165 165

FT METAL 184 184

FT METAL 187 187

FT METAL 198 198

FT METAL 201 201

SEQUENCE 371 AA; 41052 MW; 86C1AF5F87CF95C CRC64;

Query Match 82.7%; Score 67; DB 1; Length 371;

Best Local Similarity 80.0%; Pred. No. 0.0028;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 61 QKRAAYDQYGHAGVD 75

RESULT 51

Q62HD6 PRELIMINARY; PRT; 376 AA.

AC Q62HD6; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Chaperone protein DnaJ.

GN Name=dnaJ; ORFNames=BNA2325;

OS Burkholderia mallei ATCC 23344.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Burkholderia.

OX NCBI_TaxID=243160;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 23344;

RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,

RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,

RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,

RA Gwinn M.L., Haft D.H., Khouiri H., Kolonay J.F., Madupu R.,

RA Mohammed Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,

RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,

RA Zhou L., Fraser C.M.;

RT "Structural flexibility in the Burkholderia mallei genome.";

RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).

DR EMBL; CP000010; AAU49785.1; -.

SQ SEQUENCE 376 AA; 40549 MW; 9C894B4235A35D31 CRC64;

Query Match 82.7%; Score 67; DB 2; Length 376;

Best Local Similarity 80.0%; Pred. No. 0.0028;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 61 QKRAAYDQYGHAGVD 75

RESULT 52

Q63R47 PRELIMINARY; PRT; 376 AA.

AC Q63R47; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Putative DnaJ chaperone protein.

GN Name=dnaJ; ORFNames=BPS42826;

OS Burkholderia pseudomallei K96243.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Burkholderia.

OX NCBI_TaxID=272560;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K96243;

RX PubMed=15377794;

RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.M.,

RA Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,

RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,

RA Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,

RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,

RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,

RA Rabinowitz E., Rutherford K., Sanders M., Simmonds M.,

RA Songvilail S., Stevens K., Tumapa S., Vesaratchave M.,

RA Whitehead S., Yeats C., Barrell B.G., Oyatton P.C.P., Parkhill J.,

RT "Genomic plasticity of the causative agent of melioidosis,

RT Burkholderia pseudomallei.";

RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).

DR EMBL; BX571965; CHA36836.1; -.

SQ SEQUENCE 376 AA; 40596 MW; E462930B1205004E CRC64;

Query Match 82.7%; Score 67; DB 2; Length 376;

Best Local Similarity 80.0%; Pred. No. 0.0028; 2; Mismatches 0; Gaps 0;
Matches 12; Conservative 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | :
Db 61 QKRAAYDQYGHAGVD 75

RESULT 53

DNABJ_LACSK STANDARD; PRT; 383 AA.
AC O87778;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chapterone protein dnaJ.
GN Name=dnaJ;
OS Lactobacillus sakei.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1599;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=LTH681.
RX MEDLINE=20020854; PubMed=10553284;
RA Schmidt G., Hertel C., Hammes W.P.;
RT "Molecular characterisation of the dnaK operon of Lactobacillus sakei LTH681";
RL Syst. Appl. Microbiol. 22:321-328(1999).

CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- INDUCTION: By heat shock as well as salt or ethanol stress.
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC
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CC EMBL; AJ006274; CAA06942.1; -.
CC HSP; P08622; 1XBL.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; HSP40_DnaJ_pep.
CC InterPro; IPR003095; Hsp_DnaJ.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C_1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PS00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
CC Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
KW DOMAIN 6 70 J-domain.
FT DOMAIN 73 123 Gly-rich.
FT REPEAT 153 160 CXXCXGKG motif.
FT REPEAT 170 177 CXXCXGKG motif.
FT REPEAT 196 203 CXXCXGKG motif.
FT REPEAT 210 217 CXXCXGKG motif.
FT METAL 153 153 Zinc 1 (By similarity).
FT METAL 156 156 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 2 (By similarity).
FT METAL 173 173 Zinc 2 (By similarity).

FT METAL 196 196 Zinc 2 (By similarity).
FT METAL 199 199 Zinc 2 (By similarity).
FT METAL 210 210 Zinc 1 (By similarity).
FT METAL 213 213 Zinc 1 (By similarity).
SQ SEQUENCE 383 AA; 41132 MW; 3D71B3C4419EAF59 CRC64;

Query Match 81.5%; Score 66; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.0044; 0; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHGA 12
| | | | | | | | | |
Db 61 QKRAAYDQYGHGA 72

RESULT 54

Q93R26 PRELIMINARY; PRT; 386 AA.
AC Q93R26;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DnaJ.
GN Name=dnaJ;
OS Tetragenococcus halophilus (Pediococcus halophilus).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
OC Tetragenococcus.
OX NCBI_TaxID=51669;
[1]
RN RP SEQUENCE FROM N.A.
RA Fukuda D., Watanabe M., Sonezaki S., Sugimoto K., Ishizaki A.;
RT "Molecular characterization and regulatory analysis of dnaK operon of halophilic lactic acid bacterium Tetragenococcus halophilus";
RL J. Biosci. Bioeng. 0:0-0(2002).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC EMBL; AB070346; BAB63291.1; -.
CC HSP; P08622; 1XBL.
CC GO; GO:0051082; F:unfolded protein binding; IEA.
CC GO; GO:0006240; P:DNA replication; IEA.
CC GO; GO:0006457; P:protein folding; IEA.
CC GO; GO:0006986; P:response to unfolded protein; IEA.
CC InterPro; IPR000345; CytC_heme_BS.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; HSP40_DnaJ_pep.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C_1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PS00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
SQ SEQUENCE 386 AA; 41938 MW; 1F7FB80973AC02D9 CRC64;

Query Match 81.5%; Score 66; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHGA 12
| | | | | | | | | |
Db 61 QKRAAYDQYGHGA 72

RESULT 55

Q8D206 Q8D206 PRELIMINARY; PRT; 374 AA.
 ID Q8D206;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE DnaJ protein.
 GN Name=dnaJ; OrderedLocusNames=WIGBR2980;
 OS Wigglesworthia glossinidia brevipalpis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Wigglesworthia.
 OX NCBI_TaxID=36870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22297718; PubMed=12219091; DOI=10.1038/ng986;
 RA Aknan L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
 RA Akoy S.;
 RT "Genome sequence of the endocellular obligate symbiont of tsetse
 RT flies, Wigglesworthia glossinidia.";
 RL Nat. Genet. 32:402-407(2002).
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC EMBL; AB063522; BAC24444.1; -;
 DR HSP; P08622; 1BQZ.
 DR GO; GO:0051082; P:unfolded protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_p.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PRINTS; PR00625; DnaJ_CXXCXGKG; 1.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 374 AA; 41467 MW; 279CA4EC5AB020A7 CRC64;
 Query Match 80.28; Score 65; DB 2; Length 374;
 Best Local Similarity 73.3%; Pred. No. 0.0064;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAPE 15
 :|||||:|||||:
 Db 61 KGRAAYNQYGHATAFD 75
 RESULT 56
 DnaJ_RICPR STANDARD; PRT; 370 AA.
 ID Q92DYO;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chaperone protein dnaJ.
 GN Name=dnaJ; OrderedLocusNames=RP184;
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsia.
 OX NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STFAIN=Madrid E;
 RX MEDLINE=99039499; PubMed=9823893; DOI=10.1038/24094;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,

RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria.";
 RL Nature 396:133-140(1998).
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the dnaJ family.
 CC -!- SIMILARITY: Contains 1 CR domain.
 CC -!- SIMILARITY: Contains 1 J domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ235270; CAA14650.1; -;
 DR PIR; C71729; C71729.
 DR HSP; P08622; 1BQZ.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR InterPro; IPR011031; Multihem_cyt.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 FT DOMAIN 2 70 J-domain.
 FT METAL 79 105 Gly-rich.
 FT REPEAT 146 153 CXXCXGKG motif.
 FT REPEAT 163 170 CXXCXGKG motif.
 FT REPEAT 185 192 CXXCXGKG motif.
 FT REPEAT 199 206 CXXCXGKG motif.
 FT METAL 146 146 Zinc 1 (By similarity).
 FT METAL 149 149 Zinc 1 (By similarity).
 FT METAL 163 163 Zinc 2 (By similarity).
 FT METAL 166 166 Zinc 2 (By similarity).
 FT METAL 185 185 Zinc 2 (By similarity).
 FT METAL 188 188 Zinc 2 (By similarity).
 FT METAL 199 199 Zinc 1 (By similarity).
 FT METAL 202 202 Zinc 1 (By similarity).
 SQ SEQUENCE 370 AA; 41013 MW; AE6721285B4F6186 CRC64;
 Query Match 79.0%; Score 64; DB 1; Length 370;
 Best Local Similarity 73.3%; Pred. No. 0.0094;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAPE 15
 :|||||:|||||:
 Db 59 QKRAAYDREGHDAFQ 73
 RESULT 57
 Q68X13 PRELIMINARY; PRT; 370 AA.
 ID Q68X13;
 AC Q68X13;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Chaperone protein dnaJ.
 GN Name=dnaJ; OrderedLocusNames=RT0175;
 OS Rickettsia typhi.

```

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Wilington.
RX PubMed=15317790; DOI=10.1128/JB.186.17.5842-5855.2004;
RA McLeod M.P., Qin X., Karpathy S.E., Gioia J., Highlander S.K.,
RA Fox G.E., McNeill T.Z., Jiang H., Muzny D., Jacob L.S., Hawes A.C.,
RA Sodergren E., Gill R., Hume J., Morgan M., Fan G., Amin A.G.,
RA Gibbs R.A., Hong C., Yu X.-J., Walker D.H., Weinstock G.M.;
RT "Complete genome sequence of Rickettsia typhi and comparison with
RT sequences of other Rickettsiae.";
RL J. Bacteriol. 186:5842-5855(2004).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AE017197; AAU03659.1; -.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C; 1.
DR PRINTS; PR00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 370 AA; 41145 MW; 15265F965A5DD09 CRC64;

Query Match 79.0%; Score 64; DB 2; Length 370;
Best Local Similarity 73.3%; Pred. No. 0.0094;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 59 QKRAAYDQYGHAAFE 73
|||||:|||||
59 QKRAAYDQYGHAAFE 73

RESULT 58
QBRH03 PRELIMINARY; PRT; 392 AA.
ID QBRH03
AC QBRH03;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chaperone protein dnaJ.
GN OrderedLocustNames=FN0118;
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RX DOI=10.1128/JB.184.7.2005-2018.2002;
RA Kapral V., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyripides N.C., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.

Query Match 79.0%; Score 64; DB 2; Length 392;
Best Local Similarity 73.3%; Pred. No. 0.01;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 66 QKQYDQYGHAAFE 80
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66 QKQYDQYGHAAFE 80

RESULT 59
Q7P753 PRELIMINARY; PRT; 393 AA.
ID Q7P753
AC Q7P753;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=FN1498;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=ATCC 49256;
RA Karpal V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haselkorn R., Overbeek R., Kyripides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABF01000021; EAA24657.1; -.
DR HSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006280; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.

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DR EMBL; AE010525; AAL94327.1; -.
DR HSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 392 AA; 42973 MW; E62392DBE8338AD6 CRC64;

Query Match 79.0%; Score 64; DB 2; Length 392;
Best Local Similarity 73.3%; Pred. No. 0.01;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 66 QKQYDQYGHAAFE 80
|||||:|||||
66 QKQYDQYGHAAFE 80

RESULT 59
Q7P753 PRELIMINARY; PRT; 393 AA.
ID Q7P753
AC Q7P753;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=FN1498;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=ATCC 49256;
RA Karpal V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haselkorn R., Overbeek R., Kyripides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABF01000021; EAA24657.1; -.
DR HSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006280; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.

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DR	InterPro; IPR002939; DnaJ_C.
DR	InterPro; IPR001305; DnaJ_CXXCXXGXG.
DR	InterPro; IPR001623; DnaJ_N.
DR	InterPro; IPR003095; Hsp DnaJ.
DR	InterPro; IPR011031; Multihaem_cyt.
DR	Pfam; PF00226; DnaJ_1.
DR	Pfam; PF01556; DnaJ_C; 1.
DR	Pfam; PF00684; DnaJ_CXXCXXGXG; 1.
DR	PRINTS; PR00625; DNAJPROTEIN.
DR	SMART; SM00271; DnaJ; 1.
DR	PROSITE; PS00636; DNAJ_1; 1.
DR	PROSITE; PS50076; DNAJ_2; 1.
DR	PROSITE; PS00637; DNAJ_CXXCXXGXG; 1.
KW	Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT	DOMAIN 5 70 J-domain.
FT	DOMAIN 73 110 GLY-rich.
FT	REPEAT 148 155 CXXCXGXG motif.
FT	REPEAT 165 172 CXXCXGXG motif.
FT	REPEAT 187 194 CXXCXGXG motif.
FT	REPEAT 201 208 CXXCXGXG motif.
FT	METAL 148 148 Zinc 1 (By similarity).
FT	METAL 151 151 Zinc 1 (By similarity).
FT	METAL 165 165 Zinc 2 (By similarity).
FT	METAL 168 168 Zinc 2 (By similarity).
FT	METAL 187 187 Zinc 2 (By similarity).
FT	METAL 190 190 Zinc 2 (By similarity).
FT	METAL 201 201 Zinc 1 (By similarity).
FT	METAL 204 204 Zinc 1 (By similarity).
SQ	SEQUENCE 379 AA; 41279 MW; 2611F1594CDBFP58 CRC64;
Query Match 77.8%; Score 63; DB 1; Length 379;	
Best Local Similarity 73.3%; Pred. No. 0.014;	
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps	
Qy	1 QKRAAYDQGHAAPE 15 :: :
Dd	61 QKRAAYDQFGHGYD 75
RESULT 66	
Q7VVY3	
ID	Q7VVY3 PRELIMINARY; PRT; 385 AA.
AC	Q7VVY3;
DT	01-OCT-2003 (TrEMBLrel. 25, Created)
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT	01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Molecular chaperone.
GN	Name=dnaJ; OrderedLocusNames=BP2498;
OS	Bordetella pertussis.
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC	Alcaligenaceae; Bordetella.
OX	NCBI_TaxID=520;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RC	MEDLINE=28287954; PubMed=12910271; DOI=10.1038/ng1227;
RA	Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA	Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA	Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA	Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA	Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA	Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA	Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA	Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA	Shaw S., Simmonds M., Skeilton J., Squares R., Squares S., Stevens K.
RA	Unip L., Whitehead S., Barrell B.G., Maskell D.J.
RT	"Comparative analysis of the genome sequences of Bordetella pertussis"
RT	Bordetella parapertussis and Bordetella bronchiseptica.";
RL	Nat. Genet. 35:32-40(2003).
DR	EMBL; EX640418; CAB42770.1; --
DR	HSP; P08622; 1BQZ.
DR	GO; GO:0051082; F:unfolded protein binding; IEA.
DR	GO; GO:0006457; P:protein folding; IEA.

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DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR Complete proteome.
KW SEQUENCE 385 AA; 41156 MW; 8A06E4DC64B21444 CRC64;

Query Match 77.8%; Score 63; DB 2; Length 385;
Best Local Similarity 73.3%; Pred. No. 0.015;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
DB 61 OKRAAYDRYGHGVD 75

RESULT 67
Q835R5 PRELIMINARY; PRT; 389 AA.
AC Q835R5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DnaJ protein.
GN Name=dnaJ; OrderedLocustNames=E11310;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Unayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074 (2003).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AE016951; AAC01102.1; -.
DR HSSP; P08622; 1XBL.
DR TIGR; EF1310; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.

Query Match 77.8%; Score 63; DB 2; Length 385;
Best Local Similarity 73.3%; Pred. No. 0.015;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
DB 61 OKRAAYDRYGHGVD 75

RESULT 68
Q6VAY5 PRELIMINARY; PRT; 376 AA.
AC Q6VAY5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein.
GN Name=dnaJ;
OS Pseudomonas stutzeri A15.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=91504;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22964367; PubMed=14602651;
RX DOI=10.1128/AEM.69.11.6864-6874.2003;
RA Rediers H., Bonnecarrere V., Rainey P.B., Hamonts K., Vanderleyden J.,
RA De Mot R.;
RT "Development and application of a dapB-based in vivo expression
RT technology system to study colonization of rice by the endophytic
RT nitrogen-fixing bacterium Pseudomonas stutzeri A15.";
RL Appl. Environ. Microbiol. 69:6864-6874 (2003).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AY344804; AAQ22347.1; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR Complete proteome.
KW SEQUENCE 376 AA; 40132 MW; 5BB41125AB5DC0AD CRC64;

Query Match 76.5%; Score 62; DB 2; Length 376;
Best Local Similarity 78.6%; Pred. No. 0.022;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
```



```

Db      62 KRAAYDQYGHAGVD 75
RESULT 69
DNAME PSBAE
ID      DNAME PSBAE      STANDARD;      PRT;      377 AA.
AC      Q9HV44;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Chapterone protein dnaJ.
GN      Name=dnaJ; OrderedLocuNames=PA4760;
OS      Pseudomonas aeruginosa.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC      Pseudomonadaceae; Pseudomonas.
OX      NCBI_TaxID=287;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 15692 / PA01;
RX      MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA      Stover C.K.; Pham X.-O.T.; Erwin A.L.; Mizoguchi S.D.; Warren P.;
RA      Hickey M.J.; Brinkman F.S.L.; Hufnagle W.O.; Kowalik D.J.; Lagrou M.;
RA      Garber R.L.; Coltry L.; Tolentino E.; Westbrook-Wadman S.; Yuan Y.;
RA      Brody L.L.; Coulter S.N.; Folger K.R.; Kas A.; Larbig K.; Lim R.M.;
RA      Smith K.A.; Spencer D.H.; Wong G.K.-S.; Wu Z.; Paulsen I.T.;
RA      Reizer J.; Saier M.H.; Hancock R.E.W.; Lory S.; Olson M.V.;
RT      "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT      opportunistic pathogen."
RL      Nature 406:959-964(2000).
CC      -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC      the ATPase activity of dnaK (By similarity).
CC      -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC      -1- SIMILARITY: Belongs to the dnaJ family.
CC      -1- SIMILARITY: Contains 1 CR domain.
CC      -1- SIMILARITY: Contains 1 J domain.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AE004889; AAG08146.1; -.
CC      PIR; A83052; A83052.
CC      HSP; P08622; 1BQZ.
CC      InterPro; IPR002939; DnaJ_C.
CC      InterPro; IPR001305; DnaJ_CXXCXGKG.
CC      InterPro; IPR001623; DnaJ_N.
CC      InterPro; IPR008971; HSP40_DnaJ_pap.
CC      InterPro; IPR003095; Hsp_DnaJ.
CC      Pfam; PF00226; DnaJ_1.
CC      Pfam; PF01556; DnaJ_C; 1.
CC      Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC      PRINTS; PR00625; DnaJPROTEIN.
CC      SMART; SM00271; DnaJ; 1.
CC      PROSITE; PS00636; DnaJ_1; 1.
CC      PROSITE; PS00076; DnaJ_2; 1.
CC      PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
CC      KEGG; Complete proteome; DNA replication; Heat shock;
CC      Metal-binding; Repeat; Zinc.
CC      DOMAIN 5 70 J-domain.
FT      DOMAIN 73 119 Gly-rich.
FT      REPEAT 149 156 CXXCXGKG motif.
FT      REPEAT 166 173 CXXCXGKG motif.
FT      REPEAT 188 195 CXXCXGKG motif.
FT      REPEAT 202 209 CXXCXGKG motif.
FT      METAL 149 149 Zinc 1 (By similarity).
FT      METAL 152 152 Zinc 1 (By similarity).

FT METAL 166 166 Zinc 2 (By similarity).
FT METAL 169 169 Zinc 2 (By similarity).
FT METAL 188 188 Zinc 2 (By similarity).
FT METAL 191 191 Zinc 2 (By similarity).
FT METAL 202 202 Zinc 1 (By similarity).
FT METAL 205 205 Zinc 1 (By similarity).
SQ SEQUENCE 377 AA; 40260 MW; EBA30F5E71E79F4A CRC64;

Query Match 76.5%; Score 62; DB 1; Length 377;
Best Local Similarity 78.6%; Pred.No. 0.022;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15
Db 62 KRAAYDQYGHAGVD 75
RESULT 70
Q87WP1 PRELIMINARY; PRT; 380 AA.
AC Q87WP1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DnaJ protein.
GN Name=dnaJ; OrderedLocuNames=PSPT04504;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R.; Joardar V.; Lindeberg M.; Selengut J.; Paulsen I.T.;
RA Gwinn M.L.; Dodson R.J.; DeBoy R.T.; Durkin A.S.; Kolonay J.F.;
RA Madupu R.; Daugherty S.C.; Brinkac L.M.; Beanan M.J.; Haft D.H.;
RA Nelson W.C.; Daviden T.M.; Zafar N.; Zhou L.; Liu J.; Yuan Q.;
RA Khouri H.M.; Pedrosa N.B.; Tran B.; Russell D.; Berry K.J.;
RA Uterback T.R.; Van Aken S.E.; Feldblyum T.V.; D'Ascenzo M.;
RA Deng W.-L.; Ramos A.R.; Alfano J.R.; Cartinhour S.; Chatterjee A.K.;
RA Delaney T.P.; Lazarowitz S.G.; Martin G.B.; Schneider D.J.; Tang X.;
RA Bender C.L.; White O.; Fraser C.M.; Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RT Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC EMBL; AE016872; AAO57952.1; -.
CC HSP; P08622; 1EXX.
CC TIGR; PSPT04504; -.
CC GO; GO:0051082; F:unfolded protein binding; IEA.
CC GO; GO:0006260; P:DNA replication; IEA.
CC GO; GO:0006457; P:protein folding; IEA.
CC GO; GO:0006986; P:response to unfolded protein; IEA.
CC InterPro; IPR000345; CytC_heme_BS.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; HSP40_DnaJ_pap.
CC InterPro; IPR003095; Hsp_DnaJ.
CC Pfam; PF00226; DnaJ_1; 1.
CC Pfam; PF01556; DnaJ_C; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.

```


DR EMBL; AJ512795; CAD55138.1; --
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006260; P:DNA replication; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 394 AA; 43153 MW; 7711DA9A629928CD CRC64;
 Query Match 75.3%; Score 61; DB 2; Length 394;
 Best Local Similarity 66.7%; Pred. No. 0.034;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 QKRAAYDQYGHAAPE 15
 : : : : :
 Db 66 EKQYDQYGHAAPE 80

RESULT 74
 Q7PAYO PRELIMINARY; PRT; 373 AA.
 ID Q7PAYO
 AC Q7PAYO;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DnaJ protein.
 GN Name=sib orf. 471;
 OS Rickettsia sibirica.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsia; Rickettsia.
 OC NCBI_TaxID=35793;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Malek J.A., Eremeeva M.E., Dasch G.A.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABW01000001; ERAA25704.1; --
 DR HSP; P08622; LBQZ.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006260; P:DNA replication; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.

DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 373 AA; 41131 MW; 1A0C23B6E0A2A54D CRC64;
 Query Match 74.1%; Score 60; DB 2; Length 373;
 Best Local Similarity 73.3%; Pred. No. 0.048;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 QKRAAYDQYGHAAPE 15
 : : : : :
 Db 59 QKRAAYDRLGHDAFQ 73

RESULT 75
 Q92J37 PRELIMINARY; PRT; 373 AA.
 ID Q92J37
 AC Q92J37;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DnaJ protein.
 GN Name=dnaJ; OrderedLocusNames=RC0232;
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsia; Rickettsia.
 OC NCBI_TaxID=781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Malish 7;
 RX MEDLINE=21442074; PubMed=11557893; DOI=10.1126/science.1061471;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";
 RL Science 293:2093-2098(2001).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC EMBL; AEO08590; AAL02770.1; --
 DR PIR; H97728; H97728.
 DR HSP; P08622; LBQZ.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR SMART; SM00343; Znf_C2HC; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 373 AA; 41131 MW; 1A0C23B6E0A2A54D CRC64;
 Query Match 74.1%; Score 60; DB 2; Length 373;
 Best Local Similarity 73.3%; Pred. No. 0.048;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
 |||||: |||:
 Db 59 QKRAAYDRLGHDAFQ 73

RESULT 76
 Q8PMA9
 ID Q8PMA9 PRELIMINARY; PRT; 375 AA.

AC Q8PMA9; 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE DnaJ protein.

GN Name=dnaJ; OrderedLocusNames=XAC1523;

OS Xanthomonas axonopodis (pv. citri).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=92829;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=306 / ATCC 13902 / XV 101;

RX MEDLINE=2022145; PubMed=1202417; DOI=10.1038/417459a;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Canavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menco C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Seta J.A.D., Silva C., de Souza R.F.,

RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

host specificities."

RL Nature 417:459-463(2002).

CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,

CC the ATPase activity of dnaK (By similarity).

CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the dnaJ family.

DR EMBL; AB011784; AAM36392.1; -.

DR HSSP; P08622; 1BQZ.

DR GO; GO:0051082; F:unfolded protein binding; IEA.

DR GO; GO:0008457; P:protein folding; IEA.

DR InterPro; IPR000345; CytC_heme_BS.

DR InterPro; IPR002939; DnaJ_C.

DR InterPro; IPR001305; DnaJ_CXXCXGKG.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR008971; HSP40_dnaJ_pap.

DR InterPro; IPR003095; Hsp_dnaJ.

DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF01556; DnaJ_C; 1.

DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.

DR PRINTS; PR00625; DNJAJPROTEIN.

DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.

DR PROSITE; PS50076; DnaJ_2; 1.

KW Chaperone; Complete proteome; DNA replication; Heat shock;

KW Metal-binding; Repeat; Zinc.

SQ SEQUENCE 375 AA; 40317 MW; E6ACA4E70F0B8BEC CRC64;

Query Match 74.1%; Score 60; DB 2; Length 375;

Best Local Similarity 78.6%; Pred. No. 0.048;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15

|||||: |||:

Db 62 KRAYDAHGHAAFE 75

RESULT 77
 Q9APF2

ID Q9APF2 PRELIMINARY; PRT; 376 AA.

AC Q9APF2; 01-JUN-2001 (TRENBLrel. 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE DnaJ.

GN Name=dnaJ;

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP SEQUENCE FROM N.A.

RA Tai P.-M., Weng S.-F.;

RT "Sequence and Transcriptional Analysis of the grp94-dnaK-dnaJ Cluster

of the Plant Pathogenic Xanthomonas campestris pv. campestris.";

RL Gene 0:0-0(2001).

CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,

CC the ATPase activity of dnaK (By similarity).

CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the dnaJ family.

DR EMBL; AF302775; AAG53937.1; -.

DR HSSP; P08622; 1BQZ.

DR GO; GO:0051082; F:unfolded protein binding; IEA.

DR GO; GO:0006260; P:DNA replication; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR GO; GO:0006986; P:response to unfolded protein; IEA.

DR InterPro; IPR000345; CytC_heme_BS.

DR InterPro; IPR002939; DnaJ_C.

DR InterPro; IPR001305; DnaJ_CXXCXGKG.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR008971; HSP40_dnaJ_pap.

DR InterPro; IPR003095; Hsp_dnaJ.

DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF01556; DnaJ_C; 1.

DR PRINTS; PR00625; DNJAJPROTEIN.

DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.

DR PROSITE; PS50076; DnaJ_2; 1.

DR Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.

SQ SEQUENCE 376 AA; 40500 MW; 5B2FC953FCEAF2A CRC64;

Query Match 74.1%; Score 60; DB 2; Length 376;

Best Local Similarity 78.6%; Pred. No. 0.048;

Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15

|||||: |||:

Db 62 KRAYDAHGHAAFE 75

RESULT 78
 Q8PAK8

ID Q8PAK8 PRELIMINARY; PRT; 376 AA.

AC Q8PAK8; 01-OCT-2002 (TRENBLrel. 22, Created)

DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE DnaJ protein.

GN Name=dnaJ; OrderedLocusNames=XCC1475;

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach P.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
 RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorzy H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Fotwighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Medeiros J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities."
 RL Nature 417:459-463(2002).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 DR EMBL; AE012248; AA040771.1; -.
 DR HSPSP; P08622; 1BQZ.
 DR GO; GO:0051082; P:unfolded protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pdp.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 DR Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 376 AA; 40530 MW; 5B3EC953EACEAF2A CRC64;
 Query Match 74.1%; Score 60; DB 2; Length 376;
 Best Local Similarity 78.6%; Pred. No. 0.048;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 KRAAYDOYGHAAFE 15
 DB |||||:|||||
 62 KRAYDAHGHAAFE 75
 RESULT 79
 Q7UN96 PRELIMINARY; PRT; 391 AA.
 AC Q7UN96;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Chaperone protein DnaJ
 GN Name=dnaJ; OrderedLocusNames=RB8972;
 OS Rhodospirillum rubrum
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;

RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schleiner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RT strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294148; CAD76021.1; -.
 DR HSPSP; P08622; 1BQZ.
 DR GO; GO:0051082; P:unfolded protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pdp.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Complete proteome.
 SQ SEQUENCE 391 AA; 42391 MW; 49142FA922B65310 CRC64;
 Query Match 74.1%; Score 60; DB 2; Length 391;
 Best Local Similarity 78.6%; Pred. No. 0.05;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 KRAAYDOYGHAAFE 15
 DB |||||:|||||
 63 KRAYDOYGHAAFE 76
 RESULT 80
 DNAJ_CXXBU STANDARD; PRT; 374 AA.
 AC P42381;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DT Chaperone protein DnaJ.
 GN Name=dnaJ; OrderedLocusNames=CBU1289;
 OS Coccidia burnetii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Coxiellaceae; Coxiella.
 OX NCBI_TaxID=777;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nine Mile;
 RX MEDLINE=95129924; PubMed=7828937; DOI=10.1016/0378-1119(94)00687-N;
 RA Zuber M., Hoover T.A., Court D.L.;
 RT "Cloning, sequencing and expression of the dnaJ gene of Coxiella
 RT burnetii.";
 RL Gene 152:99-102(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nine Mile phase I / RSA 493;
 RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
 RA Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
 RA Nelson W.C., Ward N.L., Tettelin H., Daviden T.M., Bean M.J.,
 RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
 RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
 RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
 RT "Complete genome sequence of the Q-fever pathogen, Coxiella
 RT burnetii.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- SIMILARITY: Contains 1 CR domain.
 CC -1- SIMILARITY: Contains 1 J domain.

CC ----- This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; L36455; AAA65100.1; -;
 DR EMBL; AE016964; AA090795.1; -;
 DR PIR; I40843; I40843.
 DR HSSP; P08622; 1BQ2.
 DR TIGR; CB01289; -;
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pdp.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR InterPro; IPR011031; Multihaem_cyt.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 FT DOMAIN 5 70 J-domain.
 FT REPEAT 79 109 Gly-rich.
 FT REPEAT 146 153 CXXCXGKG motif.
 FT REPEAT 162 169 CXXCXGKG motif.
 FT REPEAT 184 191 CXXCXGKG motif.
 FT REPEAT 198 205 CXXCXGKG motif.
 FT METAL 146 146 Zinc 1 (By similarity).
 FT METAL 149 149 Zinc 1 (By similarity).
 FT METAL 162 162 Zinc 2 (By similarity).
 FT METAL 165 165 Zinc 2 (By similarity).
 FT METAL 184 184 Zinc 2 (By similarity).
 FT METAL 187 187 Zinc 2 (By similarity).
 FT METAL 198 198 Zinc 1 (By similarity).
 FT METAL 201 201 Zinc 1 (By similarity).
 FT CONFLICT 365 374 DSVKDOFFTSK -> GTV (in Ref. 1).
 SQ SEQUENCE 374 AA; 40856 MW; 7A9C3F0D140CAFB9 CRC64;

Query Match 72.8%; Score 59; DB 1; Length 374;
 Best Local Similarity 66.7%; Pred. No. 0.072;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 Db 61 RKRASYDQFGHAGVE 75

RESULT 81
 Q7NX11 PRELIMINARY; PRT; 375 AA.
 AC Q7NX11;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DE Heat shock protein dnaJ; chaperone with DnaK.
 GN Name=dnaJ; OrderedLocusNames=CV1645;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;

RA Vasconcelos A.T.R.; de Almeida D.F.; Hungria M.; Guimaraes C.T.;
 RA Antonio R.V.; Almeida F.C.; de Almeida L.G.P.; de Almeida R.;
 RA Alves-Gomes J.A.; Andrade E.M.; Araripe J.; de Araujo M.F.F.;
 RA Ascoli-Filho S.; Azevedo V.; Baptista A.J.; Bataus L.A.M.;
 RA Batista J.S.; Belo A.; van den Berg C.; Bogo M.; Bonatto S.;
 RA Bordignon J.; Brígido M.M.; Brito C.A.; Brocchi M.; Burity H.A.;
 RA Canargo A.A.; Cardoso D.D.P.; Carneiro N.P.; Carraro D.M.;
 RA Creczynski-Pasa T.B.; Cunha-Junior N.C.; Fagundes N.; Falcao C.L.;
 RA Fantiatti F.; Farias I.P.; Felipe M.S.S.; Ferrari L.P.; Ferro J.A.;
 RA Ferro M.I.T.; Franco G.R.; Freitas N.S.A.; Furlan L.R.;
 RA Gazzinelli R.T.; Gomes E.A.; Goncalves P.R.; Grangeiro T.B.;
 RA Grattapaglia D.; Grisard E.C.; Hanna E.S.; Jardim S.N.; Laurino J.;
 RA Leoi L.C.T.; Lima L.F.A.; Loureiro M.F.; Lyra M.C.C.P.;
 RA Madeira H.M.F.; Manfio G.P.; Maranhao A.Q.; Martins W.S.;
 RA di Mauro S.M.Z.; de Medeiros S.R.B.; Melssner R.V.; Moreira M.A.M.;
 RA Nascimento F.F.; Nicolas M.F.; Oliveira J.G.; Oliveira S.C.;
 RA Paixao R.P.C.; Parente J.A.; Pedrosa F.O.; Pena S.D.J.; Pereira J.O.;
 RA Pereira M.; Pinto L.S.R.C.; Pinto L.S.; Porto J.I.R.; Potrich D.P.;
 RA Ramalho-Neto C.E.; Reis A.M.M.; Rigo L.U.; Rondinelli E.;
 RA Santos E.B.P.; Santos F.R.; Schneider M.P.C.; Seunaze H.N.;
 RA Silva A.M.R.; da Silva A.L.C.; Silva D.W.; Souza E.M.; Souza K.R.L.;
 RA Simon D.; Soares C.M.A.; Soares R.B.A.; Souza E.M.; Souza K.R.L.;
 RA Souza R.C.; Steffens M.B.R.; Steindel M.; Teixeira S.R.; Urmenyi T.;
 RA Vettore A.; Wassem R.; Zaha A.; Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals
 RT remarkable and exploitable bacterial adaptability.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grp94,
 CC the ATPase activity of dnaK (By similarity).
 CC -!- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC EMBL; AE016915; AAQ5921.1; -;
 DR HSSP; P08622; 1BQ2.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006260; P:DNA replication; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR01623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pdp.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR PROSITE; PS00625; DnaJ_CXXCXGKG; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 375 AA; 40538 MW; E4D171B33B7EE433 CRC64;

Query Match 72.8%; Score 59; DB 2; Length 375;
 Best Local Similarity 66.7%; Pred. No. 0.072;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 Db 61 QKRGAYDQFGHAGVD 75
 RESULT 82
 Q8XW41 PRELIMINARY; PRT; 380 AA.
 ID Q8XW41;
 AC Q8XW41;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE PROBABLE CHAPERONE PROTEIN.
 GN Name=dnaJ; Synonym=RS04588; OrderedLocusNames=RSC2634;
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
 RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mangenot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chander M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 CC -|- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -|- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -|- SIMILARITY: Belongs to the dnaJ family.
 DR EMBL; AL646071; CAD16341.1; -;
 DR HSSP; P08622; 1BQZ.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006260; P:DNA replication; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS50076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 380 AA; 41460 MW; D340150445330340 CRC64;

Query Match 72.8%; Score 59; DB 2; Length 380;
 Best Local Similarity 71.4%; Pred. No. 0.073;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15
 Db 62 KRAAYDQYGHAGVD 75
 |||:|||||:
 KRAAYDQYGHAAFE 15
 KRAAYDQYGHAGVD 75

RESULT 83
 Q88DU3 PRELIMINARY; PRT; 375 AA.
 AC Q88DU3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DnaJ protein.
 GN Name=dnaJ; OrderedLocusNames=PP4726;
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=160488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22423060; PubMed=12534463;
 RX Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Fouts S.R., Pop M., Holmes M.,
 RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
 RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
 RA Hance I., Chris Lee P., Holtzapfle E.K., Scanlan D., Tran K.,
 RA Moazzaz A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,

RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
 RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile Pseudomonas putida KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 CC -|- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -|- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -|- SIMILARITY: Belongs to the dnaJ family.
 DR EMBL; AE016791; AAN70298.1; -;
 DR HSSP; P08622; 1BQZ.
 DR TIGR; P4726; -;
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006260; P:DNA replication; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pep.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00636; DnaJ_1; UNKNOWN_1.
 DR PROSITE; PS50076; DnaJ_2; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 375 AA; 40181 MW; BA864E707698CSAC CRC64;

Query Match 71.6%; Score 58; DB 2; Length 375;
 Best Local Similarity 71.4%; Pred. No. 0.11;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15
 Db 62 KRAAYDQYGHAGVD 75
 |||:|||||:
 KRAAYDQYGHAAFE 15
 KRAAYDQYGHAGVD 75

RESULT 84
 DnaJ_LACLA
 ID DnaJ_LACLA STANDARD; PRT; 379 AA.
 AC P35514;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chaperone protein dnaJ.
 GN Name=dnaJ; OrderedLocusNames=LL2224;
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIZO R5;
 RX MEDLINE=93194788; PubMed=8449872;
 RA van Asseldonk M., Simons A., Viesser H., de Vos W.M., Simons G.;
 RT "Cloning, nucleotide sequence, and regulatory analysis of the
 RT Lactococcus lactis dnaJ gene.";
 RL J. Bacteriol. 175:1637-1644(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21335186; PubMed=11337471; DOI=10.1101/gr.169701;
 RA Bolotin A., Wincker P., Mauger S., Jallou O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403.";

```

RL Genome Res. 11:731-753(2001).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M99413; -; NOT ANNOTATED CDS.
DR EMBL; AE006451; AK06322.1; -.
DR PIR; A47079; A47079.
DR PIR; H86902; H86902.
DR HSP; P08622; 1XBL.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; Hsp40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR PROSITE; PS00076; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 69 Gly-domain.
FT REPEAT 72 113 Gly-rich.
FT REPEAT 154 161 CXXCXGKG motif.
FT REPEAT 171 178 CXXCXGKG motif.
FT REPEAT 197 204 CXXCXGKG motif.
FT REPEAT 211 218 CXXCXGKG motif.
FT METAL 154 154 Zinc 1 (By similarity).
FT METAL 157 157 Zinc 1 (By similarity).
FT METAL 171 171 Zinc 2 (By similarity).
FT METAL 174 174 Zinc 2 (By similarity).
FT METAL 197 197 Zinc 2 (By similarity).
FT METAL 200 200 Zinc 2 (By similarity).
FT METAL 211 211 Zinc 1 (By similarity).
FT METAL 214 214 Zinc 1 (By similarity).
FT CONFLICT 94 94 G -> S (in Ref. 1).
FT CONFLICT 164 164 A -> R (in Ref. 1).
SQ SEQUENCE 379 AA; 40671 MW; 399CA4EDCB7067B6 CRC64;

Query Match 71.6%; Score 58; DB 1; Length 379;
Best Local Similarity 91.7%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
DB 60 QKRAAYDQYGE 71

RESULT 85
Q93066 PRELIMINARY; PRT; 379 AA.
AC Q93066;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein DnaJ.

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GN Name=dnaJ;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RA Seerensen K.I., Kilestrup M.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AF280940; AA669493.1; -.
DR HSP; P08622; 1XBL.
DR GO; GO:0051082; F:unfolding protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; Hsp40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
SQ SEQUENCE 379 AA; 40840 MW; 082AFB84DCA6641D CRC64;

Query Match 71.6%; Score 58; DB 2; Length 379;
Best Local Similarity 91.7%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
DB 60 QKRAAYDQYGE 71

RESULT 86
DnaJ_CAUCR
ID DnaJ_CAUCR STANDARD; PRT; 385 AA.
AC P22305;
DT 01-AUG-1991 (Rel. 19, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocNames=CC0011;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Uterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

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RN  SEQUENCE OF 1-193 FROM N.A.
RP  MEDLINE=90264295; PubMed=2345134;
RA  Gomes S.L., Guber J.W., Shapiro L.;
RT  "Expression of the Caulobacter heat shock gene dnaK is developmentally
RL  controlled during growth at normal temperatures.";
RJ  J. Bacteriol. 172:3051-3059(1990).
CC  -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC  the ATPase activity of dnaK (By similarity).
CC  -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -1- SIMILARITY: Belongs to the dnaJ family.
CC  -1- SIMILARITY: Contains 1 CR domain.
CC  -1- SIMILARITY: Contains 1 J domain.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AB005676; AA021999.1; -.
DR  EMBL; M55224; AAA62724.1; -.
DR  PIR; C87250; C87250.
DR  HSSP; P08622; 1BQZ.
DR  TIGR; CC0011; -.
DR  InterPro; IPR002939; DnaJ_C.
DR  InterPro; IPR001305; DnaJ_CXXCXGKG.
DR  InterPro; IPR001623; DnaJ_N.
DR  InterPro; IPR008971; HSP40 DnaJ_pap.
DR  InterPro; IPR003095; Hsp_DnaJ.
DR  Pfam; PF00226; DnaJ_1.
DR  Pfam; PF01556; DnaJ_C; 1.
DR  Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR  PRINTS; PR00625; DnaJPROTEIN.
DR  SMART; SM00271; DnaJ; 1.
DR  PROSITE; PS00636; DnaJ_1; 1.
DR  PROSITE; PS00076; DnaJ_2; 1.
DR  PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW  Chaperone, Complete proteome; DNA replication; Heat shock;
KW  Metal-binding; Repeat; Zinc.
FT  DOMAIN 1 70
FT  REPEAT 77 118 Gly-rich.
FT  REPEAT 148 155 CXXCXGKG motif.
FT  REPEAT 165 172 CXXCXGKG motif.
FT  REPEAT 187 194 CXXCXGKG motif.
FT  REPEAT 201 208 CXXCXGKG motif.
FT  METAL 148 148 Zinc 1 (By similarity).
FT  METAL 151 151 Zinc 1 (By similarity).
FT  METAL 165 165 Zinc 2 (By similarity).
FT  METAL 168 168 Zinc 2 (By similarity).
FT  METAL 187 187 Zinc 2 (By similarity).
FT  METAL 190 190 Zinc 2 (By similarity).
FT  METAL 201 201 Zinc 1 (By similarity).
FT  METAL 204 204 Zinc 1 (By similarity).
FT  METAL 22 23 AF -> RV (in Ref. 2).
FT  CONFLICT 22 23 P -> S (in Ref. 2).
FT  CONFLICT 58 58 GVNGPQG -> AGQRGN (in Ref. 2).
FT  CONFLICT 71 77 RQNSA -> AVQR (in Ref. 2).
FT  CONFLICT 110 114 PPAAMT -> IPRHEP (in Ref. 2).
FT  CONFLICT 142 147 SPVCG -> QPLCLR (in Ref. 2).
FT  CONFLICT 161 166 R -> P (in Ref. 2).
FT  CONFLICT 173 173 RGCP -> AA (in Ref. 2).
FT  CONFLICT 185 188
SQ  SEQUENCE 385 AA; 40965 MW; 930181194622B2C5 CRC64;

Query Match 71.6%; Score 58; DB 1; Length 385;
Best Local Similarity 83.3%; Pred. No. 0.11;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAA 12
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Db 59 QKRAAYDRFGHA 70
RESULT 87
ID Q67853 PRELIMINARY; PRT; 386 AA.
AC Q67853;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Heat shock protein, DnaJ.
OS Name=dnaJ; ORFNames=STH505;
GN Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IAM14863;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsui T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Complete genome sequence of an uncultured bacterium Symbiobacterium
RT thermophilum".
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
DR  EMBL; AF006840; BAD39490.1; -.
DR  GO; GO:0006457; P:protein folding; IEA.
DR  GO; GO:0006986; P:response to unfolded protein; IEA.
DR  InterPro; IPR002939; DnaJ_C.
DR  InterPro; IPR001305; DnaJ_CXXCXGKG.
DR  InterPro; IPR001623; DnaJ_N.
DR  InterPro; IPR008971; HSP40 DnaJ_pap.
DR  InterPro; IPR003095; Hsp_DnaJ.
DR  InterPro; IPR011031; Multihaem_cyt.
DR  Pfam; PF00226; DnaJ; 1.
DR  Pfam; PF01556; DnaJ_C; 1.
DR  Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR  PRINTS; PR00625; DnaJPROTEIN.
DR  SMART; SM00271; DnaJ; 1.
DR  PROSITE; PS00636; DnaJ_1; 1.
DR  PROSITE; PS00076; DnaJ_2; 1.
DR  PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW  Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
SQ  SEQUENCE 386 AA; 42541 MW; E579253D353BA3FF CRC64;

Query Match 71.6%; Score 58; DB 2; Length 386;
Best Local Similarity 76.9%; Pred. No. 0.11;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAA 13
|||||:|||||
Db 64 EKRRARYDQFGHAA 76
RESULT 88
ID Q7S1F9 PRELIMINARY; PRT; 414 AA.
AC Q7S1F9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Name=NCU07414.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
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[illegible]

DE Chaperone protein dnaJ.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93014224; PubMed=1383161;
 RA Anzola J., Luft B.J., Gorgone G., Peltz G.;
 RT "Characterization of a Borrelia burgdorferi dnaJ homolog.";
 RL Infect. Immun. 60:4965-4968(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93211279; PubMed=8459764;
 RA Tilly K., Hauser R., Campbell J., Ostheimer G.J.;
 RT "Isolation of dnaJ, dnaK, and grpE homologues from Borrelia burgdorferi and complementation of Escherichia coli mutants.";
 RL Mol. Microbiol. 7:359-369(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ATCC 35210 / B31;
 RC MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
 RA Frazer C.M., Caejens S., Huang M.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
 RA Gwin M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
 RA Richardson D.L., Peterson M., van Vugt R., Palmer N., Adams M.D.,
 RA Salzberg S.L., Hanson M., J. F. Uterback T.R., Matthey L., McDonald L.A.,
 RA Gocayne J.D., Weidman J.F., Uterback T.R., Matthey L., McDonald L.A.,
 RA Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
 RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.";
 RL Nature 390:580-586(1997).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- INDUCTION: By heat shock.
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- SIMILARITY: Contains 1 CR domain.
 CC -1- SIMILARITY: Contains 1 J domain.
 CC -----
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 CC -----
 DR EMBL; M97914; AAA22925.1; -;
 DR EMBL; M96847; AAA22948.1; -;
 DR EMBL; AE001154; AAC66888.1; -;
 DR PIR; D70164; D70164.
 DR HSSP; PB8622; 1BQ2.
 DR TIGR; BB0517; -;
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS0076; DnaJ_2; 1.
 DR PROSITE; PS00387; DnaJ_CXXCXGKG; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
 FT DOMAIN 4 69 J-domain.
 FT DOMAIN 75 87 Gly-rich.

FT REPEAT 148 155 CXXCXGKG motif.
 FT REPEAT 165 172 CXXCXGKG motif.
 FT REPEAT 187 194 CXXCXGKG motif.
 FT REPEAT 201 208 CXXCXGKG motif.
 FT METAL 148 148 Zinc 1 (By similarity).
 FT METAL 151 151 Zinc 1 (By similarity).
 FT METAL 165 165 Zinc 2 (By similarity).
 FT METAL 168 168 Zinc 2 (By similarity).
 FT METAL 187 187 Zinc 2 (By similarity).
 FT METAL 190 190 Zinc 2 (By similarity).
 FT METAL 201 201 Zinc 1 (By similarity).
 FT METAL 204 204 Zinc 1 (By similarity).
 FT CONFLICT 143 143 T -> A (in Ref. 1).
 FT CONFLICT 296 352 Missing (in Ref. 2).
 FT CONFLICT 344 352 KLPENLGKE -> NFLKTKAKN (in Ref. 1).
 SQ SEQUENCE 364 AA; 40498 MW; BE1748AC9BC34082 CRC64;
 Query Match 70.4%; Score 57; DB 1; Length 364;
 Best Local Similarity 64.3%; Pred. No. 0.16;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 2 KRAAYDOYGHAAPE 15
 Db 61 KRAKYDRFGHSAPE 74
 ID Q661A4 PRELIMINARY; PRT; 364 AA.
 AC Q661A4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Heat shock protein.
 GN Name=dnaJ-1; ORFNames=BG0528;
 OS Borrelia garinii PBI.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 NCBI_TaxID=290434;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PBI;
 RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
 RA Schulte-Spechtel U., Wilske B., Suehnel J., Platzer M.;
 RT "Comparative analysis of the Borrelia garinii genome.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 DR EMBL; CP000013; AAU07167.1; -;
 DR GO; GO:0008457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR InterPro; IPR008162; Pyrophosphatase.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS0076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 DR PROSITE; PS00387; DnaJ_CXXCXGKG; 1.
 KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 364 AA; 40612 MW; 80559C67EAB3DA CRC64;
 Query Match 70.4%; Score 57; DB 2; Length 364;
 Best Local Similarity 64.3%; Pred. No. 0.16;


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Query Match 70.4%; Score 57; DB 1; Length 369;
Best Local Similarity 90.9%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGH 12
Db 62 KRAAYDQFGHA 72
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|:|:|:|:|:|

RESULT 95
Q634M8 PRELIMINARY; PRT; 371 AA.
AC Q634M8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chapterone protein.
GN Name=dnaJ; ORFNames=BTZK4060;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU16209.1; -.
SQ SEQUENCE 371 AA; 40349 MW; BPDFC56797916010 CRC64;

Query Match 70.4%; Score 57; DB 2; Length 371;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 QKEAAYDQYGH 12
Db 60 QKRAQYDQFGHA 71
|||||:|||||
|:|:|:|:|:|

RESULT 96
Q6WNG0 PRELIMINARY; PRT; 371 AA.
AC Q6WNG0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DnaJ protein.
GN Name=dnaJ; OrderedLocusNames=Bdi1296;
OS Bdellovibrio bacteriovorus
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; BX842649; CAE79192.1; -.
DR GO; GO:0042649; CAE79192.1; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
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DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_dep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR PRINTS; PR00625; DnaJ_CXXCXGKG; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 371 AA; 40776 MW; 00P83F727437C58F CRC64;

Query Match 70.4%; Score 57; DB 2; Length 371;
Best Local Similarity 71.4%; Pred. No. 0.16;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKEAAYDQYGH 14
Db 62 QKRAQYDRFGHDAF 75
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|:|:|:|:|:|

RESULT 97
Q730M2 PRELIMINARY; PRT; 371 AA.
AC Q730M2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=BCE4394;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01."
RL Nucleic Acids Res. 32:977-988(2004).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AS017278; AAS43295.1; -.
DR TIGR; BCE4394; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_dep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR PRINTS; PR00625; DnaJ_CXXCXGKG; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
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SQ SEQUENCE 371 AA; 40363 MW; D9B362A82B670555 CRC64;
Query Match 70.4%; Score 57; DB 2; Length 371;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
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DB 60 QKRAQYDQFGH 71

RESULT 98
Q818F0 PRELIMINARY; PRT; 371 AA.
AC Q818F0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chaperone protein dnaJ.
GN OrderedLocuNames=BC4311;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC EMBL; AE017012; AAP11224.1; -.
DR HSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; DnaJ_C.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF06684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 371 AA; 40465 MW; 8832D121033F6A27 CRC64;
Query Match 70.4%; Score 57; DB 2; Length 371;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
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DB 60 QKRAQYDQFGH 71

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RESULT 99
Q81LS3 PRELIMINARY; PRT; 371 AA.
AC Q81LS3; Q6HT78; Q6KMG8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocuNames=BA4538, BAS4212, GBA44538;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilestone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.,
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AE017038; AAP28247.1; -.
DR EMBL; AE017334; AAT33659.1; -.
DR HSP; P08622; 1BQZ.
DR TIGR; BA4538; -.
DR TIGR; GBA44538; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF06684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.

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KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 371 AA; 40363 MW; FFD75679791170C CRC64;

Query Match 70.4%; Score 57; DB 2; Length 371;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
Db 60 QKRAQYDQFGHA 71

RESULT 100

Q6HDK8
ID Q6HDK8 PRELIMINARY; PRT; 371 AA.
AC Q6HDK8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chaperone protein.
GN Name=dnaJ; OrderedLocusNames=BT9727.4050;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with groE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AE017355; AAT63523.1; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR011305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_dep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00150; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 371 AA; 40363 MW; FFD75679791170C CRC64;

Query Match 70.4%; Score 57; DB 2; Length 371;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
Db 60 QKRAQYDQFGHA 71

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